AJ132436 Arabidops BD243013 Enzyme. 7 AR444995 Sequence BT002987 Arabidops AX50655 Sequence AX51428 Sequence AX51428 Sequence AR528430 Sequence AR528430 Sequence AR5760281 Spinam sat AF700955 Pisum sat AF700357 Sequence AZ004307 Sequence AZ004307 Sequence AZ00873 Arabidops AZ00873 Sequence

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THE UNIVERSITY OF BRISTOL

OS Phaseolus coccineus (scarlet runner bean)

PD 25-UUN-2002

PF 11-UUN-1999 GB 981281.8,15-UUL-1998 GB 9815404.0 PI
STEBHEN GREGORY THOWAS, PETER HEDDEN, ANDREW LEONARD PHILLIPS PC
CLINNS/04, A01H5/00, CLINN/15, CLINN/19, CLINN/10, CLINS/10, PC
CLINNS/09, CLINNS/00, CLINNS/00, CLINNS/10, CLINNS/10, PC
CLINNS/09, CLINNS/00, CLINNS/00, CLINNS/10, CLINNS/10, PC
CLINNS/09, CLINNS/00, CLINNS/00, CLINNS/10, CLINNS/10, CLINNS/10, PC
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Phaseolus coccineus
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosida; eurosida I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Phaseolus
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/organism="Phaseolus coccineus"
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Patent: JP 2002518005-A 1 25-JUN-2002;
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AY085539
ATH132435
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   (bases 1 to 1318)
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JP 2002518005-A/1
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ACCESSION
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KEYWORDS
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CQ899251 Sequence
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AY588978 Nerium ol
AY5894292 Nerium ol
AX302041 Cucurbita
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AJ302041 Cucurbita
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AR452811 Sequence
AR852817 Sequence
AB81373 Olida ang
AR852817 Sequence
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Db 1021 AGCTGATAATAGGCTTGCCCCTTTCCAGAATCTGCTGCTGATTAACCAAACACACCCTT 1080 Qy 1081 CAAATTCCACTCATTTTACGCACGTGTTATTACCCCAATTTTCTTTTCTTTTCT 1140 Db 1081 CAAATTCCACTCATTTTACGCACGTGTTATTACCCCAATTTTCTTTTCTTTTCC 1140 Qy 1141 TGTGTCTGTCTAGGTTTCAAACAGTTGACTCTAGTATATAGAAAATGAATAGGT 1200 Qy 1201 TAAGATGTTTATCATTTTCTTTTTCTTTTCATTTGACATATATAGAAATGAATAGGT 1200 Qy 1201 TAAGATGTTTATCATTTTCTTTTTCTTTTCATTTCATCTAGTGTAACAGTTGGTCTCAACTT 1260 Qy 1201 TAAGATGTTTATCATTTTTTTTTTTTTTTTTTTTTTTTT	RESULT 2 AR44491 LOCUS LOCUS LOCUS Sequence 1 from patent US 6670527. ACCESSION AR444991 VERSION KEYWORDS SCHOOL ONGANISM Unknown. ONGANISM Unknown. ONGANISM TITLE ORGANISM TITLE TITLE GIBbereallin 2-oxidaes JOURNAL THE University of Bristol; Bristol; GBX; LOCATION/QUALIfiers SOURCE 1. 1318 AUTHORS GBX; LOCATION/QUALIFIERS AUTHORS FEATURES 1. 1318 AUTHORS The University of Bristol; Bristol; GBX; LOCATION/QUALIFIERS AUTHORS AUTHORS The University of Bristol; Bristol; AUTHORS AUT	DAA TCT TCT TCT CAG	Qy 121 CAAGTCCACGCCCTTGTTCACGGGGATTCCTGGGTCCACGCACCCCGATGCCAA 180 Db 121 CAAGTCCACGCCTTGTTCACGGGATTCCTGGGTCGACCCCGATGCCAA 180 Qy 181 GAATCTCATAGTGAACGCCTGTAGGGACTTCTGGGTCTCTGAACCTTGTGAACCATGGTGT 240 Db 181 GAATCTCATAGTGAACGCCTGTAGGGACTTCTGGGTTTTCAAGACTTGTGGTGT 240 CA 241 TCCATTGGAGTTAATGGCCAATTTAGAAAACGGGCCTTCTGGGTTTTTAAAAATCTCA 300 Db 241 TCCATTGGAGTTAATGGCCAATTTAGAAAACGGGCCCTCAGGTTCTTTAAAAAATCTCA 300 Qy 301 GTCCGAGAAGACGGCCCCAATTTAGGAAAACGGGCCCTCAGGTTCTTTAAAAAATCTCA 300 Qy 301 GTCCGAGAAAGACGGCCCCCCGACCCTTTCGGCTATGGTAGCAAGAGGATTGG 360 Qy 361 CCCAAACGAGAGCTGGTCCCCCCCGACCCTTTCGGCTATGGTAGCAAGAGGATTGG 360 Qy 361 CCCAAACGGTGATGGGTCCCCCCCCCCCCCCCCCCCCCC
Best Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0; Matches 1318; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Operation 0; Indels 0; Gaps 0; Indels Indels	Qy 241 TCCATTGGAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAATCTCA 300 Db 241 TCCATTGGAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAATCTCA 300 CA 301 GTCCGAGAAAGAGCTGGTCCCCCCCCCCCTCAGGTTCTTTTAAAAATCTCA 300 CA 301 GTCCGAGAAAGAGCTGGTCCCCCCCCCCTTTCGGCTATGGTAGCAAGAGGATTGG 360 CA 301 GTCCGAGAAAGAGCTGGTCCCCCCCCCCCTTTCGGCTATGGTAGCAAGAGGATTGG 360 CA 361 CCCCAAAGGGTGATGGGTCGAATACCTCCTCCTCCTCAACCCTGATGTTAT 420 CA 361 CCCCAAACGGTGATGGGTCGAATACCTCCTCCTCCTCTCATGTTAT 420 CA 361 CCCCAAACGGTGATTTCCGAGAAAAACCTCCTCCTCTCTATTTCAGGGCGTGGTGGA 480 CA 421 CTCACCCAAATTACAGCAGTGAAATACTTCCCAACACTCATTTCAGGGCGGTGGTGGA 480 CA 481 GAACTACATTACAGCAGTGAAAAATCCTCATCATTTCAGGGCGGTGGTGGA 480 CA 481 GAACTACATTACAGCAGTGAAAAATCTCTCATCATTTCAGGGCGGTGGTGGA 540 CA 481 GAACTACATTACAGCAGTGAAAAATCTCTCATTTCAGGGCGGTGGTGGGGGGGG	Oy 541 GTTGGGGATAAGCAGAATACGTTAAGCAGGTTGCTGAAGGATGAAAGTGATTC 600	Db 721 ATCTGGCTGCAALCTCCCAGAGGCTTCGGCTTCCCCCCCGGACGACCAGAC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 GTCCGAGAAAGACAGAGCTGGTCCCCCCGACCTTTCGGCTATGGTAGCAAGAGGATTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    601 GTGCTTCAGGTTGAACCACTACCCGCCTTGCCCTGAGGTGCAAGCACTGAACCGGAATTT
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                                                                                                                                                                                                                          Score 1316.4;
Pred. No. 0;
0; Mismatches
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                                                                                                                                                                                                                                               Best Local Similarity 99.5
Matches 1317; Conservative
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AJ132438.1 GI:4678585
A 2-oxidase; galoxi gene.
Phaseolus coccineus
Phaseolus coccineus
Busaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons;
coside; eurosids I; Pabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                 960
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Submitted (18-JAN-1999) Phillips A.L., Plant Sciences, IACR Long
Ashton Research Station, Long Ashton Research Station, Bristol,
BS41 9AF, UR
                                              TGTAAAACATAGGGTTTTTGGCTGACAAACGAAGTCAAGGTTATCAATGATCTACTTTGG
                                                                                                                    AGGACCAGCGTTGAGTGAAAATATAGCACCTTTACCTTCAGTGATGATAAAAGGAGGAGGA
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                                                                                                 AGGACCAGCGTTGAGTGAAATATATGCACCTTTACCTTCAGTGATGTTAAAAGGAGAGGA
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Molecular cloning and functional expression of gibberellin oxidases, multifunctional enzymes involved in gibberellin deactivation
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Phaseolus coccineus mRNA for GA 2-oxidase, gene ga2oxl
AJ132438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 96 (8), 4698-4703 (1999)
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/organism="Phaseolus coccineus"
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1. .1318
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/product="GA 2-oxidase"
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/db_xref="taxon:3886"
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/gene="ga2ox1"
68. .1066
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/protein id="BAD9950".1"
/brotein id="BAD9950".1"
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/translation="
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Pred. No. 3.7e-281;
0; Mismatches 93; Indels
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Matches 1214; Conservative C
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Vigna angularis VaGA20xA1 mRNA for gibberellin 2-oxidase, complete
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Submitted (08-JUN-2004) Masatoshi Nakajima, The University of Submitted (08-JUN-2004) Masatoshi Nakajima, The University of Tokyo, Debt. Appl. Biol. Chem., Fac. of Agriculture; 1-1-1 Yayoi, Bunkyo, Tokyo, 13-8677, Japan (E-mail:nkim@pog11.ch.a.u-tokyo.ac.jp, Tel:81-3-5841-5192, Fax:81-3-5841-8025)
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                                                                                                                                                     1045 TAGGCTTGCCCCTTTCGAGAAATCTGCTACTGATTAAGCAAACACACCCTTCAAATTCTA 1104
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Bormatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
phaseolus.

        28
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        187

        61
        ACGCCTTGTTCACGGGGATTCCTGTGGTCGACCTCACGCACCCCGATGCCAAGAATCTC
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865 TAGGGTTTTGGCTGACACAACGAAGTCAAGGTTATCAATGATATACTTTGGAGGACCAGC 924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 75.8%; Score 999; DB 6; Length 999; Best Local Similarity 100.0%; Pred. No. 1e-251; Matches 999; Conservative 0; Mismatches 0; Indels
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                                                                                           GCTGATAATAGGCTTGCCCCTTTCCAGAAATCTGCTGCTGATTAACCAAACACACCCTTC 1081
                                                                                                                                                                                                                                              TCTTTTCCTGTGTCTGTCTAGGTTTCAAACAGTTGACTCTACTTGACATATATAGAAAAT 1192
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Nerium oleander

Nerium oleander

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta, eudicotyledons; core eudicotyledons; asterids, lamiids, Gentianales, Apocynaceae; Apocynoideae;

Wrightieae, Nerium.

1 (bases ito 1406

1 (bases 1, Garcia-Martinez, J.L. and Lopez-Diaz, I. Isolation, characterization and multi-site polyadenylation of genee GA 2-oxidases and GA 2-oxidases in Nerium oleander
                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished

2 (bases 1 to 1406)
Ubeda-Tomas, S., Garcia-Martinez, J.L. and Lopez-Diaz, I.
Ubeda-Tomas, S., Garcia-Martinez, J.L. and Lopez-Diaz, I.
Direct Submission
Submitted (02-APR-2004) Instituto de Biologia Molecular de Plantas,
CSIC/Universidad Politecnica de Valencia, Avda de los Naranjos sn,
Valencia 46022, Spain
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AYS88978 1406 bp mRNA linear PLN 01-MAY-200
Nerium oleander gibberellin 2 oxidase (GA2ox3) mRNA, complete cds.
AYS88978
                                     999 AGTTTCTACAAAGAGTTCACATGGTGGGAATACAAGAAGGCTGCGTACGCGTCAAGGCTA
                                                                                                                                                                                          TTTTGGGTGTGTGTATCTAGGTTCCAAACAGTTGACTTTACTTGAGATATATAGAAAT
                                                                                                                                 1059 GCGGATAATAGACTCGGCCCTTTTGAGAATCTGCTGCTGATTAAGGAGGCAAAGTGTGT
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/note="GA 2-oxidase; NoGA2ox3"
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Logusch, S.J., Piller, K.J., Rao, S., Ream, J.E. and Baerson, S.R. Methods for controlling globerellin levels
Patent: US 6723897-A 62 20-APR-2004;
Monsanto Technology, LLC; St. Louis, WO
Location/Qualifiers
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                                                                                                                                                                                            Length 1359
                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                          67.8%; Score 893.8; DB 6;
84.9%; Pred. No. 5.3e-224;
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/protein id="AP192094.1"
//brotein id="AP192094.1"
//db_xref="G1:51011366"
//d
                                                             PLN 30-APR-2005
                                                                                                                                                                                                  Nerium oleander
Nerium oleander
Nerium oleander
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiids; Gentianales; Apocynaceae; Apocynoideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ubeda-Tonas, S., Garcia-Martinez, J.L. and Lopez-Diaz, I. Ubeda-Tonas, S., Garcia-Martinez, J.L. and Lopez-Diaz, I. Direct Submission Submitted (18-ARR-2004) Institute de Biologia Molecular y Celular de Plantas, Consejo Superior de Investigaciones Cientificas (CSIC), Universidad Politecnica de Valencia, Avda. de los Naranjos s/n, Valencia 46022, Spain Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCACATTATTCCCGGGTGTTCCATTGATAGACCTCTCGAAACCTGACTCGAAACACCTC 120
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1 (bases 1 to 1245)

1 (bada-Tomas,S., Garcia-Martinez,J.L. and Lopez-Diaz,I.
1solation, characterization and multi-site polyadenylation
20-oxidases and GA 2-oxidases in Nerium oleander
Unpublished
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2-oxidase 2 mRNA, complete cds
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larity 67.9%; Pred. No. 6.6e-111;
Conservative 0; Mismatches 316;

    1245
    /organism="Nerium oleander"
/mol_type="mRNA"
    /db_xref="taxon:63479"

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/product="GA 2-oxidase 2"
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                                                                Gaps
   Length 1406;
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                                                             Indels
   DB 15;
Score 484.6; DB 15;
Pred. No. 3.2e-116;
0; Mismatches 278;
Query Match
Best Local Similarity 70.4%;
Matches 677; Conservative
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PLASLMQGEERSLYKRFTWFBYKRSAVNSRLADNRLVPFERIAAS."
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                                                                                                                              function="2-oxoglutarate dependent dioxygenase"
                                                                                                                                                                                                                                                                                                                                                                     35.1%; Score 462.2; DB 15; Length 1383; 68.7%; Pred. No. 2.5e-110; ive 0; Mismatches 293; Indels 3;
                                                                                                                                                /codon_start=1
/product="Gibberellin 2-oxidase"
               tissue type="root tips"
'dev stage="7 day old seedling"
[. .1383
   clone="2beta-WS2"
                                                                       /gene="ga2ox"
43. .1008
                                                                                                             gene="ga2ox"
                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 68.7
Matches 651; Conservative
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Cucurbita maxima partial mRNA for Gibberellin 2-oxidase (ga2ox
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AGACTCAATCACTACCCACCTATCCTGACCTTCAAGAACTGCCATGGCAGGAATTTAATT
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Submitted (19-JUN-2001) Lange T., Botanical Institute, TU
Braunschweig, Mendelsschnstr. 4, D-38106 Braunschweig, GERMANY
related entry AJ315662.
Location/Qualifiers
                                                       ATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTGATGGCGGAGGGGTTGGGG
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                                                                                          GTATCATCAGTAAAGAAATGGCTTGTGAATACTTGAATTAATGGCAGAAGGTTTGAAT
                                                                                                                                ATAAGGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGATTCGTGCTTC
                                                                                                                                                                 AGGITGAACCACTACCCCCTTGCCCTGAGGTGCAAGCACTGAA---CCGGAATTTGGTT
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/mol_type="mRNA"
/cultivar="Riesenmelone, gelb genetzt"
/db_xref="caxon:3661"
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Gibberellin biosynthesis in young seedlings of
Unpublished
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AJ315663.1 GI:32127336
ga20x gene; gibberellin 2-oxidase.
Cucurbita maxima (winter squash)
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TITLE
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A for gibberellin 2-oxidase 1, complete
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    TCTGCAGCATTCTACTCTGGGATTCCATTGATAGACCTCTCTGCACCAGATGCTAAACAA 167
                                                                                                                                                         CTCATTGTCAAAGCTTGTGAAGAACTCGGATTCTTTAAGGTTGTCAAACATGGTGTCCCC 227
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                                                                                 CTCATAGTGAACGCCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCCA
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/gene="ga2ox"
/function="2-oxoglutarate dependent gibberellin
dioxygenage"
/codon_start=1
/codon_start=1
/producl="gibberellin 2-oxidase"
/producl="dxC83090.1"
/protein_id="dxC83090.1"
/db_xref="di:2712365"
/db_xref="GA:08GUE8"
/db_xref="GA:08GUE8"
/db_xref="mintorcyfreMel:08GUE8"
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/db_xref="min
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Direct Submission
Submitted (14-DEC-2000) Lange T., Botanical Institute, Dept. Plant
Submitted (14-DEC-2000) Lange T., Braunschweig, Mendelssohnstr. 4,
Braunschweig, D-38106, GERMANY
Braunschweig, D-38106, GERMANY
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Spermatophyta, Magnoliophyta, eudicotyledons; core eudicotyledons,
rosids, eurosids I, Cucurbitales, Cucurbitaceae, Cucurbita.
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GIGAAGCATAGGGTTTTGACAAACAGCTCGAAGTCAAGGGTTTCAATGATCTACTTCGGT
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                                                                                                                         GGACCAGCGTTGAGTGAAAATATAGCACCTTTACCTTTCAGTGATGTTAAAAGGAGAGGAG
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Cucurbita maxima mRNA for gibberellin 2-oxidase (ga2ox gene)
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Unpublished
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Pred. No. 1.7e-109;
0; Mismatches 295; Indels
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/dev stage="developing embryos"
1. .1308
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/mol_type="mRNA"
/cultivar="Riesenmelone, gell
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ga20x gene; gibberellin 2-oxidase.
Cucurbita maxima (winter squash)
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649; Conservative
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Best Local S:
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727 777 787 837 847 897 907 957 964

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MacMillan, J., Ward, D.A., Phillips, A.L., Sanchez-Beltran, M.J., Gaskin, P., Lange, T. and Hedden, P. Gibberellin biosynthesis from gibberellin Al2-aldehyde in endosperm and embryos of Marah macrocarpus Plant Physiol. 113 (4), 1369-1377 (1997)
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I; Cucurbitales, Cucurbitaceae, Marah.
                                                                                                     608 TGTTTTCAGGCTCAATCACTATCCCCCTTGTCCCGAGATTCAACAATTCAGTGACAATAA
                                                                                                                                                               TTTGGTTGGGTTTGGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTAACAG
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                                                                                                                                                                                                                                             CACATCTGGCTTGCAAATCTGTCTCACAGATGGCACTTGGGTTTCAGTCCCACCTGATCA
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GTTGGGGATAAGGCAGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGATTC
                                    548 ATTAAATATTCATCCTAGGAACGTTTTCAGTAAACTTCTAATGGACGAAAAGAGTGACTC
                                                                                GTGCTTCAGGTTGAACCACTACCCGCCTTGCCCTGAGGTGCAAGCACTGA---ACCGGAA
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YFGGPPLSEKIAPLASLMEGEESLYEEFTWFESYKKSAYKTRLADNRLVLFEKVAAS"
                                                                                                                                       2 (bases 1 to 1292)
Sakane,M., Nakajima,M. and Yamaguchi,I.
Direct Submission
Submitted (188-00T-2003) Masayuki Sakane, University of Tokyo,
Applied Biological Chemistry; Yayoi 1-1-1, Bunkyo-ku, Tokyo
III-30012, Japan (E-mail:m-sakane@pgrl.ch.a.u-tokyo.ac.jp,
UKL:http://pgrl.ch.a.u-tokyo.ac.jp/, Tel:81-3-5841-5158 (ex.25158),
Fax:81-3-5841-8025)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiids; Solanales; Solanaceae; Nicotiana.
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0; Mismatches 355; Indels
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                                                                 Molecular cloning of GA 2-oxidase in BY-2 Unpublished
                                                                                                                                                                                                                                                                                                                                      /organism="Nicotiana tabacum"
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/cfl_line="BY-2"
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                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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75. .1073
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20-FEB-2004

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Unclassified.

1 (bases 1 to 1352)
Allen,S.M., Kinney,A.J., Rafalski,J.A., Orozco,E.M. Jr.,
Allen,S.M., Kinney,A.J., Lee,J.-M., Lohman,K.N., Rendina,A.R.,
Sakai,H., Weng,Z., Caimi,P.G., Fang,Y., Shen,J.B.J., Zoughi,I.L.,
Anderson,S.L., Shi,J., Lu,G., Helentjaris,T.G. and Li,C.P.
Plant metabolism genes
Patent: US 6677502-A 13 13-JANN-2004;
E.I. du Pont de Nemours and Company and Pioneer Hi-Bred
International, Wilmington, DE
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TGCCAAGAATCTCATAGTGAACGCCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAACCA
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                                                                                                                                                                                                               32.7%; Score 430.8; DB 6;
larity 65.7%; Pred. No. 4.7e-102;
Conservative 0; Mismatches 332;
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       dev_stage="immature seed"
                                                                         /product="dioxygenase"
/protein_id="CAA70330.1"
/db_xref="G1:1666096"
/db_xref="GOA:004162"
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Length 1352;

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414 505 474 553

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354 452 414 512 474

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                TGCCAAGAATCTCATAGTGAACGCCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAACCA
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Allen,S.M., Kinney,A.J., Rafalski,J.A., Orozco,E.M. Jr.,
Miao,G.-H., Pamodu,O.O., Lee,J.-M., Lohman,K.N., Rendina,A.R.,
Sakai,H., Weng,Z., Caimi,P.G., Fang,Y., Shen,J.B.J., Zoughi,I.L.,
Anderson,S.L., Shi,J., Lu,G., Helentjaris,T.G. and Li,C.P.
Plant metabolism genes
Patent: US 6677502-A 5 13-JAN-2004;
B.I. du Pont de Nemours and Company and Pioneer Hi-Bred
International, Wilmington, DE
Location/Qualifiers
                                                                               674 TGACTCTATTTTCAGGGTGAATCATTACCCTGCTTGTCCTGAAATGACTCTGAATGATGATCA
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AR452817

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New isolated plant gibberellin 2-oxidase enzymes and nucleic acids, used to produce transgenic plants with improved or altered growth characteristics.
                                                                Gibberellin 2-oxidase; PcGA2ox1; runner bean; 2-beta-hydroxylation; inactivation; growth inhibition; ss.
                                                                                                            Location/Qualifiers
68. .1066
/*tags a /
/product= "Gibberellin 2-oxidase PCGA2ox1"
/bransl_except= (pos:1058. .1063, aa:Ala)
                                            Runner bean gibberellin 2-oxidase PcGA2oxl cDNA.
                                                                                                                                                                                                                                                                              Phillips AL;
                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 1; 42pp; English
                                                                                                                                                                                                                               98GB-00012821.
                                                                                                                                                                                                                                                                              Thomas SG, Hedden P,
                                                                                                                                                                                                                                                           UYBR-) UNIV BRISTOL.
                                                                                                                                                                                                                                                                                                 WPI; 2000-097742/08.
P-PSDB; AAY58597.
                                                                                                                                                                                                                               12-JUN-1998;
15-JUL-1998;
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Aeb67733 Rice geno Ada70120 Rice gene Adk00081 Rice cDNA Aeb67784 Rice geno

Result

This sequence represents cDNA encoding a runner bean gibberellin (GA) 2oxidase, PcGAZOXI. This enzyme is a GA 2-beta-hydroxylase that acts on
C19-GAB and for which 2-beta-hydroxylation is its only activity.
C19-GAB and for which 2-beta-hydroxylation of a GA results in a biologically
inactive product, and is the most important route for GA metabolism in
plants, ensuring that the active hormones do not accumulate in plant
c19-GAB ender the concentration of bloactrom plants so that
c19-GAB ender the concentration of bloactrom plants so that
c2-endered to reduce the concentration of bloactrom plants so that
c3-endered to reduce the concentration of bloactrom plants so that
c4-endered to reduce the concentration of bloactrom plants so that
c5-endered to reduce the concentration of bloactrom plants so that
c6-endered to reduce the concentration of such as enhancing lodgingc7-endered and prain yield in cereals, improving seedling quality,
c7-endering the growth of amenity grasses, reducing shoot growth in orchard
c8-endered price growth of amenity grasses, reducing shoot growth in orchard
c8-endered price growth of amenity grasses, reducing shoot growth in orchard
c8-endered sprouting, reduce shoot growth in hedging plants, inhibit
c8-eversibility in the development or germination of seeds and reduce shoot
c9-exidase (claimed) to promote plant growth, (e.g., to improve fruit set
c9-exidase (claimed) to promote plant growth, (e.g., to improve fruit set
c9-exidase (claimed) to promote plant growth, (e.g., to improve fruit set
c9-extidese (claimed) in species citrus fruits and pears), improve skin
c10-exidase growth in seedless grasse, citrus fruits and pears), improve malting yields and quality in cereals (particularly in cereals yield and earliness in celery and rhubarb,
c10-exidase growth in woody species
c10-exidase growth in woody species
c10-exidase growth in woody species

Sequence 1318 BP; 358 A; 296 C; 282 G; 382 T; 0 U; 0 Other;

420 61 AACAACCATGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAAACCATT 120 AACAACCATGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAAACCATT 120 180 240 240 TCCATTGGAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCA 300 300 GTCCGAGAAAGACAGAGCTGGTCCCCCCGACCTTTCGGCTATGGTAGCAAGAGGATTGG 360 Greceagadadadadedederececedadecentresecratestadadadadadanse 420 480 480 540 GTTGGGGATAAGGCAGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGATTC 600 CAAGTCCACGCCCTTGTTCACGGGATTCCTGTGGTCGACCTCACGCACCCCGATGCCAA GAATCTCATAGTGAACGCCTGTAGGGACTTCGGCTTCTTCAGGCTTGTGAACCATGGTGT TCCATTGGAGTTAATGGCCAATTTAGAAACGAGGCCCTCAGGTTCTTAAAAAATCTCA cccaaaceerearercerresercearacercercercaacaccaaccrearerrar CTCACCCAAATCACTTTGCATTTTCCGAGAAAATCCTCATCATTTCAGGGCGGTGGTGGA GAACTACATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTGATGGCGGAGGG GAATCTCATAGTGAACGCCTGTAGGGACTTCGGCTTTCAAGCTTGTGAACCATGGTGT CTCACCCAAATCACTTTGCATTTTCCGAGAAAATCCTCATCATTTCAGGGCGGTGGTAGA Gaps ; 0 DB 3; Length 1318; 0; Indels Query Match 100.0%; Score 1318; Best Local Similarity 100.0%; Pred. No. 0; Matches 1318; Conservative 0; Mismatches 61 361 121 121 241 241 181 181 301 301 361 421 481 481 541 421 셤 δ a 8 셤 ò g ઠે 셤 8 8 ò a ò g ò 셤

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à i	21	ATCTGGCTTGCAAATCTGTCTCACAGATGGCACTTGGGTTTCAGTCCCACTGATCAGAC	780
g D	N		780
ò	ω	TTCCTTTTTCATCATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAAG E	840
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\$ 8	841	TGTAAAGCATAGGGTTTTGGCTGACACAAGGTCAAGGTTATCAATGATCTACTTTGG : 	900
3 8	7 0	, 00141104171407140714171170740717074074074747474	
<u>8</u>	901	VOI AGGACCAGCGITGAGIGAMAATAITAGGACCITTAGCITTAGGIGAITAGAGAGGAGAG	96
ò	961	GIGITIGIACAAAGAGITCACAIGGIGIGAAIACAAGAAGGCIGCGIACACIICAAGGCI	102
a	961	GIGITTGTACAAAGAGTTCACATGGTGTGTGAATACAAGAAGGCTGCGTACACTTCAAGGCT	102
à	1021	AGCTGATAATAGGCTTGCCCTTTCCAGAAATCTGCTGCTGATTAACCAAACACGCCTT	106
g	1021	AGCTGATAATAGGCTTGCCCCTTTCCAGAAATCTGCTGCTGATTAACCAAACACCTT .	รั
à	1081	CAAATTCCACTCATTTTACGCACGTGTTATTACCCCAATTTTCTTTC	114
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ò	1141	TGTGTCTGTCTAGGTTTCAAACAGTTGACTTGACATAGATAG	120
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QQ	1261	aacgcaactctagttacaaaaaaaaaaaaaaaaaaaaaa	18
RESU ADT6 ID	ULT 2 62692 ADT62692	LT 2 8692 ADT62692 standard; DNA; 999 BP.	
χų	ADT62692;		
žË	13-JAN-20	05 (first entry)	
X E	DNA encod	ling Phaseolus coccineus gibberellin 2-oxidase.	
1222	DNA plasm expressic gibberell	id; transfer DNA; T-DNA; Agrobacterium Ti plasmid; transgene; n cassette; transgenic plant; transgenic; plant; in 2-oxidase; ds.	
\$ 8 \$	Phaseolus	coccineus.	
Z Z	WO2004092	390-A2.	
£ ₽ ¥	28-OCT-20	. 104.	
Z Z X	09-APR-20	04; 2004WO-US011000.	

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The present invention relates to a DNA plasmid comprising a transfer DNA (T-DNA) comprising an Agrobacterium Ti plasmid first border region linked to at least one transgene linked to an Agrobacterium Ti plasmid second to at least one transgene linked to an Agrobacterium Ti plasmid second border region, and located in the DNA plasmid outside of the T-DNA is a plant expression cassette comprising a plant cell non-lethal negative contain vector backbone DNA, a method for reducing the copy number of a transgene in a plant cell, and a transgenic plants that do not contain vector backbone DNA, a method for reducing the copy number of a cransgene in a plant cell, and a transgenic plant produced by the method. The DNA plasmid comprises the expression cassette comprising a promoter that functions in plant cells operably linked to a plant cell non-lethal copy number of a constitutive selection marker gene. The promoter expresses the linked non-lethal negative promoter. The promoter expresses the linked non-lethal negative selection marker gene comprises a plant hormone chosynthetic pathway gene of signalling gene, or metabolic interference substrate-diverting gene of signalling gene, or metabolic interference from antibiotic resistance and herbicide resistance. The transgene of agronomic interest. The plant hormone comprises a transgene of agronomic interest. The plant hormone of blosynthetic pathway gene is selected from gibberelitic acid pathway.
                                                                                                                                                                                                        New DNA plasmid comprising a T-DNA comprising an Agrobacterium Ti plasmid first border region linked to a transgene linked to an Agrobacterium Ti plasmid second border region, useful for enhancing production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genes, cytokinin pathway genes, auxin pathway gene, ethylene pathway genes, and absolaic acid pathway genes. The plasmid is useful for enhancing the production of commercially viable transgenic plants. The present sequence represents DNA encoding Phaseolus coccineus gibberellin
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09-APR-2003; 2003US-0461459P
                                                    (MONS ) MONSANTO TECHNOLOGY
                                                                                                     Gilbertson L, Krieger E,
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                                                                                                                                                                                                                                                                                             transgenic plants.
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Sequence 999 BP; 263 A; 221 C; 249 G; 266 T; 0 U; 0 Other;

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                                                                                                                     ACGCCCTTGTTCACGGGGATTCCTGTGGTCGACCTCACGCACCCCGATGCCAAGAATCTC
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                                                   ATGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAAACCATTCAAGTCC
                          Gaps
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                         0; Indels
75.8%; Score 999; DB 13; L 100.0%; Pred. No. 1.9e-266; Ative 0; Mismatches 0;
                          Matches 999; Conservative
              Local Similarity
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                                                                     TTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTGTAAAG
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                                                     188 ATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTGATGGCGGAGGGGTTGGGG
                                                                                                                                   481 ATAAGGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGATTCGTGCTTC
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                        TCCTTTTTCATCATCATGTTGGTGACACTCTTCAGGTAATGACTAATGGGAGGTTTAAAAGT
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/product= "GA 2-oxidase 1 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes a gibberellic acid 2-oxidase 1 protein describes which is used in the method of the invention. The specification describes methods for the inhibition and control of gibberellic acid levels. Gibberellic acid levels may be inhibited or controlled by use of a chimeric expression construct expressing a RNA or protein which suppresses the gibberellin biosynthetic pathway sequence, diverts substrate from the pathway, or degrades pathway substrates or products. The methods uses copalyl diphosphate synthase, 3beta-hydroxylase, 2-oxidase, phytoene synthase, C-20 oxidase, and a 2beta-hydroxylase polynucleotides to achieve this. The method is used to control seed gibberellin biosynthetic pathway and restoration of normal seed gibberellin biosynthetic pathway and restoration of normal seed germination, in transgenic plants from the plants produced are gibberellin deficient, and have shortened hypocotyl and/or epicotyl phenotypes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 ACCATGGTTGTTCTGTCTCAGCCAGCATAAACCAGTTTTTCCTTCTGAAAACATGCAAG 158
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                                                                                                                                                                                                                                                                       Obtaining transgenic plant useful for controlling seed germination and seedling growth comprises transgene comprising a sequence expressing altered levels of an essential hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cccaagrcacagrcarrircagagaaggrccrcagaarrrcagggggggggaa
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                                                                                                                                                   SJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 67.8%; Score 893.8; DB 3; Length 1359; Best Local Similarity 84.9%; Pred. No. 3.5e-237; Matches 1069; Conservative 1; Mismatches 158; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1359 BP; 340 A; 305 C; 304 G; 409 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                     Claim 45; Page 248; 267pp; English
                                                                                                                                                 Heck GR,
99WO-US018066
                                        98US-0096111P
99US-0137977P
                                                                                                                                                                       Rao S, Ream JE;
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                                                                                                                                                 Elich TD,
                                                                                                                                                                                                             WPI; 2000-224351/19.
P-PSDB; AAY84099.
                                                                                                      (MONS ) MONSANTO CO
10-AUG-1999;
                                        10-AUG-1998;
07-JUN-1999;
                                                                                                                                               Brown SM, Piller KJ,
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TTTTGGGTGTGTGTATCTAGGTTCCAAACAGTTGACTTTACTTGAGATATATAGAAAT 1238
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                                                                                                                                           579 GGGATAACGCAGAGGAATGTGTTGAGTAGGTTGCTGAAGGATGAGAAGAGTGATYCTTGC
                                                                                                                                                                                     TTCAGGTTGAACCACTACCCGCCTTGCCCTGAGGTGCAAGCACTGAAC---CGGAATTTG
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                                                                                                    GGGATAAGGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGATTCGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soybean; ss; plant; plant metabolism; GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate synthase; Dioxygenase; Ent-Kaurene Synthase A; GA-20 oxidase; Gtlibberellin 3-beta hydroxylase; Riboflavin specific deaminase; Ethylene response factor; Acyl-CoA thioesterase II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAACAGTTGGTCTCAACTTCCCTTTTCCTCAATTGTCAATGGAACGCAACTCTAGTTACA
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The method involves producing transgenic plants having a phenotype of reduced seed germination and reduced early seedling growth, then restoring seed germination and early seedling growth by treating plants with an appropriate compound when conditions are favourable. The method is useful to control seed germination and/or early seedling growth in gricultural production so that unfavorable environmental conditions normally reducing agronomic output can be avoided and yields increased. Plants also demonstrate increased uniformity of germination, emergence and seedling vigor, so increasing yields at harvest. The method is especially useful in crop plants such as e.g. canola, soybean, cotton, etc., and is also useful in storage and transport of seeds to reduce premature germination which may affect agronomic or food quality of the seeds. The present sequence is soybean GA 2-oxidase 1 cDNA
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                                                                                                                                                                                                                                                                                                                                                                            Control of gibberellin levels in plants useful to avoid unfavorable conditions in crops to increase yields, using transgenic plants having reduced seed germination and early seedling growth then treatment to restore these properties.
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1; Mismatches 158;
amino acid"
                                                                                                                                                                                                                                                    Kishore GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 45; Page 92-93; 155pp; English.
/note= "Xaa = any
                                                                                                                                                                                                                                                  Heck GR,
                                                                                                                          99US-00371307
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                                                                                                                                                                                                                                                                          Rao S, Ream JE;
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                                                                                                                                                                                                          (BROW/) BROWN
                                                                                                                          10-AUG-1999;
                                                                                02-MAY-2002
                                                                                                                                                                                                                                                                        Piller KJ,
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combinant DNA construct comprising the polymentages activity, appearing as Authorized acquence encoding a polypoptide having GTP cyclohydrolase (1/3,4-dihydroxy-2-butanone-4-phosphate synthase activity, appearing as ADM94266. Also included are a vector comprising the polymucleotide, a cell comprising the polymucleotide operably linked to combinant DNA construct, transforming a cell with the polymucleotide, a cell comprising transforming a plant cell with the polymucleotide and regenerating a plant from the transformed plant cell), a plant comprising transforming a plant comprising transforming a plant cell with the polymucleotide and regenerating a plant from the transformed plant cell), a plant comprising the recombinant DNA construct. Also disclosed as new are mucleic acid (CDNA) fragments and assembled contigs encoding plant metabolism proteins (CDNA) fragments and assembled contigs encoding plant metabolism proteins (CDNA) fragments and assembled contigs encoding plant metabolism proteins chosen from GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate companies, ploxygraguase, Riboflavin specific deaminase, Ethylene response the reduction of transporter. PMP70 ABC transporter GNN20-like, P-Glycoprotein I, P-Glycoprotein I, P-Glycoprotein I, P-Glycoprotein Dave I benefit and protein CCC cond. The mucleic acid fragments may be used to create transgenic plants where the polypeptides are present at higher or lower levels than normally cond. The polympetides can be used to probe Southern blots containing restriction endounclease-treated genomic DNAs of a set of physically mapping genes and as markers for transfering parent and sophyperides containing restriction endounclease-treated genomic DNAs of a set of molymprophism (RFLP). It can also be used to probe Southern blots containing restriction endounclease-treated genomic DNAs of a set of molymprophism (RFLP). It can also be used to probe southern blots containing restriction and source primer of properties of the mutation as gequence primer in conjuncti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate synthase nucleic acid and proteins, useful for creating transgenic plants where polypeptides are present at higher or lower levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1, Kinney AJ, Rafalski JA, Orozco EM, Miao G, Famodu OO;
Lohman KN, Rendina AR, Sakai H, Weng Z, Caimi PG, Fang Y;
Zoughi IL, Anderson SL, Shi J, Lu G, Helentjaris TG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to an isolated polynucleotide comprising a
ABC transporter GCN20-like; P-glycoprotein I; P-glycoprotein 3; P-glycoprotein ATPGP; P-glycoprotein HVMDR2; ABC transporter; PMP70 ABC transporter; MRP4 ABC transporter; transgenic.
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PIONEER HI-BRED INT INC.
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99US-0146650P.
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15-DEC-1999;
21-DEC-1999;
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Shen JB,
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                                                                                                              55 AACAACAACAACCATGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAA
                                                                                                                                                 146 AACAACAAGAAAATGGTGTTGTTGTCCAAAGCAACAGAACAGAATACTCCTACATTAA
                                                                                                                                                                                      115 ACCATTCAAGTCCACGCCCTTGTTCACGGGATTCCTGTGGTCGACCTCACGCACCCCGA
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                                      DB 12; Length 1352;
                                                                           15;
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Sequence 1352 BP; 439 A; 255 C; 243 G; 415 T; 0 U; 0 Other;
                                                                           Indels
                   Score 430.8; DB 12;
Pred. No. 1.2e-108;
                                  32.7%;
al Similarity 65.7%;
665; Conservative
                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                        235
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nucleotide sequence encoding a polygeptide having GTP cyclohydrolase

II/3,4-dihydroxy-2-butanone-4-phosphate synthase activity, appearing as

EC II/3,4-dihydroxy-2-butanone-4-phosphate synthase activity, appearing as

EC MDM94266. Also included are a vector comprising the polymucleotide, a

recombinant DNA construct comprising the polymucleotide operably linked

to at least one regulatory sequence, transforming a cell with the

EC to at least one regulatory sequence, transforming a cell with the

EC polymucleotide and regenerating the recombinant DNA construct,

producing a plant (comprising transforming a plant cell with the

EQ polymucleotide and regenerating a plant from the transformed plant cell,

EQ polymucleotide and regenerating a plant from the transformed plant cell),

a plant comprising the recombinant DNA construct and a seed comprising

the recombinant DNA construct. Also disclosed as new are nucleic acid

(cDNA) fragments and assembled contigs encoding plant metabolism proteins

chosen from GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate

Synthase, bloxygenase, Ent-Kaurene Synthase A, GA-20 oxidase, Gibberellin

Synthase, Dioxygenase, Rhr-Kaurene Synthase A, GA-20 oxidase, Gibberellin

Hown A, II-COA thioesterase II, ABC transporter GCN20-like, P-

HVMDR2, ABC transporter, PMP70 ABC transporter and MRP4 ABC transporter.

The mucleic acid fragment may be used to create transgenic plants where

the polypeptides are present at higher or lower levels than normal or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate synthase nucleic acid and proteins, useful for creating transgenic plants where polypeptides are present at higher or lower levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM, Kinney AJ, Rafalski JA, Orozco EM, Miao G, Famodu OO;
, Lohman KN, Rendina AR, Sakai H, Weng Z, Caimi PG, Fang Y;
JB, Zoughi IL, Anderson SL, Shi J, Lu G, Helentjaris TG;
                                                                                                                                                                                            Soybean; 88; plant; plant metabolism; GTP cyclohydrolase II/3, 4-dihydroxy-2-butanone-4-phosphate synthase; Dioxygenaes; Ent-Kaurene Synthase A; GA-20 oxidase; Gdbberellin 3-beta hydroxylase; Riboflavin specific deaminase; Ethylene response factor; Acyl-CoA thioesterase II; P-glycoproter GTOXIO-like; P-glycoprotein I; P-glycoprotein 3; P-glycoprotein PPBP; P-glycoprotein HVMDR2; AGC transporter; PMP70 ABC transporter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated polynucleotide comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; SEQ ID NO 5; 186pp; English
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                         ADM94205 standard; cDNA; 1365 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0143401P.
99US-0143412P.
99US-0146650P.
99US-0170906P.
99US-0172946P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-JUL-2000; 2000US-00614912
                                                                                                                                                           Soybean Dioxygenase cDNA #1
                                                                                                               (first entry)
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P-PSDB; ADM94206.
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21-DEC-1999;
21-DEC-1999;
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cell types or in developmental stages in which they are not normally found. The polynucleotides can be used as probes for genetically and physically mapping genes and as markers for traits linked to those genes. The nucleic acid fragments may be used as restriction fragment length colymorphism (RFLP). It can also be used to probe Southern blots containing restriction endonuclease-treated genomic DNAs of a set of individuals representing parent and progeny of a defined genetic cross. The nucleic acid fragments may also be used as hybridisation probes against PCR amplification products generated from the mutation population using the mutation tag sequence primer in conjunction with an arbitrary genomic site primer. The peptides can also be used to immunise animals to produce polyclonal or monoclonal antibodies with specificity for peptides or produce polyclonal or monoclonal antibodies with specificity for peptides or proteins comprising the amino acid sequences. Antibodies are useful for detecting the polypoptides in altu in cells or in vitro in cell ~ 452 212 234 TGGTGTTCCATTGGAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAA 294 354 414 512 474 560 Grrgaacagrracargrcrrcrgrgaggaagarggcargrgagarrcrrgagrrgarggc 620 594 621 AGAAGGGTTGAAGATTCAGCAAAAGGATGTTTAGCAAGCTTCTAATGGATAAACAAAG 680 654 174 TGCCAAGAATCTCATAGTGAACGCCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAACCA 333 regrererecarecaacerarareceaarrecaarareaacerreaarrerrerr 295 ATCTCAGTCCGAGAAAGACAGAGCTGGTCCCCCCGACCCTTTCGGCTATGGTAGCAAGAG TGATTCGTGCTTCAGGTTGAACCACTACCCGCCTTGCCCTGAGGTGCAAGCACTGAACCG aacaacaacaaaaareererrerrerceaaccaacaacaacaaraarerrerracarraa 213 GAACTGCATGCCAACCAAATTTTCCTCAACAATTCCCATAGTGGACCTCTCCAAACCTGA GGAGGGGTTGGGGATAAGGCAGAGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAG reactionariances de la respectación de la respectaci 115 ACCATTCAAGTCCACGCCCTTGTTCACGGGGATTCCTGTGGTCGACCTCACGCACCCCGA 393 grcacrcaargaaaagaaaaagraagaccrcccaarccarrrgggrarggragcaagaa 453 AATTGGACACAATAGGGACGTTGGTTGGATTGAGTACCTTCTTCTCAACACACCAATCAAGA 55 AACAACAACAACCATGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAA 35 GATTGGCCCAAACGGTGATGTCGGTTGGGTCGAATACCTCCTCCTCAACACCCAACCCTGA 415 TGTTATCTCACCCAAATCACTTTGCATTTTCCGAGAAAATCCTCATCATTTCAGGGCGGT GGTGGAGAACTACATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTGATGGC Gaps Score 429.2; DB 12; Length 1365; Pred. No. 3.3e-108; 0; Mismatches 333; Indels 15; Sequence 1365 BP; 448 A; 258 C; 244 G; 415 T; 0 U; 0 Other; Query Match 32.6%; Best Local Similarity 65.6%; Matches 664; Conservative ' 153 273 561 681 175 235 475 595 셤 셤 유 qq ઠે 임 ð 셤 ò g ò 셤 ò 셤 ઠે g ò ò ò δ

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Best Local Similarity 66.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents cDNA encoding an Arabidopsis thaliana gibberellin (GA) 2-oxidase, PcGA2ox2. This enzyme is a GA 2-beta-hydroxylation at the acts on C19-GAs and for which 2-beta-hydroxylation is its only activity. Hydroxylation at the 2-beta position of a GA results in a biologically inactive product, and is the most important route for GA metabolism in plants, ensuring that the active hormones do not accumulate in plant issues. The nucleic acids can be used to transform plants so that gibberellin 2-oxidase can be constitutively over-expressed or otherwise enhanced to reduce the concentration of bioactive GAs in the plants and therefore to inhibit plant growth. Growth inhibition is useful in many agricultural and horticultural applications such as enhancing lodging-resistance and grain yield in cereals, improving seedling
                                              894
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861 TGACAAATCCTTTTTTATTAACGTTGGTGATTCTCTTCAGGTTATGACAAATGGAAGGTT 920
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                                                                                         921 CCGAAGTGTGAGACACAGAGTGTTGGCAAATGGGTTCAAGTCCAGGCTTTCAATGATTTA
                                                                                                                                     CTTTGGAGGACCAGCGTTGAGTGAAATATAGCACCTTTACCTTCAGTGATGTTAAAAGG
                                           835 TAAAAGTGTAAAGCATAGGGTTTTGGCTGACACAAGGAAGTCAAGGTTATCAATGATCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2-oxidase, AtGA2ox2; 2-beta-hydroxylation; inactivation;
                                                                                                                                                                                                                                                                                                                                                      1098 AAGATTATCTAAAAATAGACTTGAACATTTTGAAAGAATTGCAGCTTCGTAA 1149
                                                                                                                                                                                                                                                                                                                           AAGGCTAGCTGATAATAGGCTTGCCCCTTTCCAGAAATCTGCTGCTGATTAA 1066
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/product= "Gibberellin 2-oxidase AtGA2ox2"
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/*tag= a
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quality, reducing the growth of amenity grasses, reducing shoot growth in orchard and ornamental trees, improving tolerance to cold, drought and infection, and increasing yields (by the diversion of assimilates from vegetative to reproductive organs). The nucleic acids may also be used to induce male and/or female sterility (by expression in floral organs), prevent pre-larvest sprouting, reduce shoot growth in hedging plants, inhibit reversibility in the development or germination of seeds and reduce shoot growth in commercial wood species. Antisense constructs of the nucleic acids can also be used to transform plants to reduce the expression of GA 2-oxidase (claimed) to promote plant growth, (e.g., to improve fruit set and growth in seedless grapes, citrus fruits and lears), improve skin texture and fruit shape in apples, increase stem length and therefore yield in sugar cane, increase yield and earliness in celery and rhubarb, improve malting yields and quality in cereals (particularly barley), and increase growth in woody species
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TGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAGCTGATAATAGGCTTGCCCCTTTC 1045
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                                    GAGCAGGAATATGGCTICTICGGCTIGCTCAGICTCTIAAAAACCGGGCCGGICCA
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                                                                                  976 GCACCATIGCCAIGCCTTGICCCTGAGCAAGATGATIGGCTTTACAAAGAATTCACTTGG
                                                                                                                                                    TGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAGCTGATAATAGGCTTGCCCCTTTC
                             GCACCTTTACCTTCAGTGATGTTAAAAGGAGAGAGTGTTTGTACAAAGAGTTCACATGG
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Pred. No. 3.3e-107;
0; Mismatches 306; Indels 3;
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26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
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                                                                                                                                                                                                         GCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTGTAAAGCATAGGGTTTTGGCTGAC 865
                                                                                                                                                                                                                                                                           ACAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACCAGCGTTGAGTGAAATATA 925
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                     CCACAGATAATCTCAGTGCTAAGATCTAATAACACGGGGGTCTTCAAATCTGTGTGAAA
                                                                                                                                        GATGGCACTTGGGTTTCAGTCCCACCTGATCAGACTTCCTTTTTCATCATGTTGGTGAC
                                                                                                                                                           GCTCTTCAGGTTATGACTAACGGGAGGTTCAAGAGTGTTAAACCACAGGGTCTTAGCCGAT
                                                                                                                                                                                                                                                                                                    ACAAGGAGATCGAGGATTTCAATGATATATTTCGGCGGACCGCCATTGAGCCAGAAGATC
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 CCTTGCCCTGAGGTGCAAGCACTGAACCGGAATTTGGTTTGGGTTTTGGGAGCACACAGAC
                                                                     CCACAGATAATTTCTGTCTTAAGATCTAACAGCACATCTGGCTTGCAAATCTGTCTCACA
                                                                                                                                                                                                                                                                                                                                              GCACCTTTACCTTCAGTGATGTTAAAAGGAGAGGAGTGTTTGTACAAAGAGTTCACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gibberellic acid; copalyl diphosphate synthase; 3beta-hydroxylase; 2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase; seed germination; seedling growth; gibberellin biosynthetic pathway; transgenic plant; hypocotyl; epicotyl; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "gibberellic acid 2-oxidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGAAACAACCTCTCTCAATCATAAAACCC 1018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGAAATCTGCTGCTGATTAACCAAACACAC
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99US-0137977P.
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Ream JE;
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07-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.
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                                                                                                                                                                                                                                                                                      Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
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                                                                                                                                                                                                         Hou Y;
I, Zou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1026 BP; 274 A; 242 C; 251 G; 259 T; 0 U; 0 Other;
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Zhu
                                                                                                                                                                                                        Glazebrook J, Goff
Whitham S, Xie Z,
                                                                                                                                                                                                                                                                                                                                                                              Claim 6; SEQ ID NO 223; 899pp; English.
                                                                                                                                                                      (SYGN ) SYNGENTA PARTICIPATIONS
                                                                                                   22-JUN-2001; 2001WO-IB001105
                                                                                                                                      22-JUN-2001; 2001WO-IB001105
                                                                                                                                                                                                         κ'n
                                                                                                                                                                                                         Cooper B
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Katagiri F, Quan S,
Arabidopsis thaliana
                                                                                                                                                                                                                                                           WPI; 2003-175290/17.
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                                 WO2003000898-A1
                                                                                                                                                                                                                                                                                                                                              expression
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nes 622;
                                                                   03-JAN-2003
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Best Local S:
Matches 622,
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959 TACTITIGEAGGICCACCATIGAGIGAGAAAATAGTACCATTAICTICACTTAIG---AAA 1015
                                                                                                                                                                                                                                                                                                             1016 GGAAAAGAAAGCTTATACAAAGAGTTTTACGTGGTTCGAGTATAAAAATTTAACCTATGCT 1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to control of gibberellin (GA) levels in plants. The method involves producing transgenic plants having a phenotype of reduced seed germination and reduced early seedling growth, then restoring seed germination and early seedling growth by treating plants with an appropriate compound when conditions are favourable. The method is useful to control seed germination and/or early seedling growth in agricultural production so that unfavorable environmental conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Control of gibberellin levels in plants useful to avoid unfavorable conditions in crops to increase yields, using transgenic plants having reduced seed germination and early seedling growth then treatment to rescore these properties.
                                                             TTTAAAAGTGTAAAGCATAGGGTTTTTGGCTGACACAAGGAGGTCAAGGTTATCAATGATC
                                                                                                                                                      899 Trrcgaagrergaagcacagagrrrrgacaaarggarrraagreragacrercaargarr
                                                                                                                                                                                               TACTTTGGAGGACCAGCGTTGAGTGAAAATATAGCACCTTTACCTTCAGTGATGTTAAAA
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                                        GATCAGACTTCCTTTTTCATCTTGGTGACGCTCTACAGGTAATGACTAATGGGAGG
779 AACAATACTTCAGGCCTTCAGATTTTTCTTAGAGATGGAAACTGGATTTCAGTCCCACCT
                                                                                                                                                                                                                                                                                                                                                                        1076 TCAAGATTGGCTGATAATAGGCTTGGACATTTTGAGAGAATTGTTGCTTCATAA 1129
                                                                                                                                                                                                                                                                                                                                                      TCAAGGCTAGCTGATAATAGGCTTGCCCCTTTCCAGAAATCTGCTGCTGATTAA 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; transgenic plant; seed germination; seedling growth; 2-oxidase 2; enzyme; GA; soybean; gene; ss.
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/product= "GA 2-oxidase 2 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 45; Page 94-95; 155pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
149. .1129
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P-PSDB; AAE24922.
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Piller KJ,
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                                                                                         The present sequence encodes a gibberellic acid 2-oxidase 2 protein sequence, which is used in the method of the invention. The specification describes methods for the inhibition and control of gibberellic acid levels. Gibberellic acid levels may be inhibited or controlled by use of a chimeric expression construct expressing a RNA or protein which suppresses the gibberellin biosynthetic pathway sequence, diverts substrate from the pathway, or degrades pathway substrates or products. The methods uses copalyl diphosphate synthase, 3beta-hydroxylase, oxidase, phytoene synthase, C-20 oxidase, and a 2beta,3beta-hydroxylase polymucleotides to achieve this. The method is used to control seed germination and seedling growth especially to require gene products of gibberellin biosynthetic pathway and restoration of normal seed germination, in transgenic plants. The plants produced are gibberellin deficient, and have shortened hypocotyl and/or epicotyl phenotypes
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    seedling growth comprises transgene comprising a sequence expressing altered levels of an essential hormone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 424.8; DB 3; Length 1403; Pred. No. 5.6e-107;
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1403 BP; 440 A; 269 C; 261 G; 433 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches 327; Indels
                                                             Claim 45; Page 250; 267pp; English.
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normally reducing agronomic output can be avoided and yields increased. Plants also demonstrate increased uniformity of germination, emergence and seedling vigor, so increasing yields at harvest. The method is especially useful in crop plants such as e.g. canola, soybean, cotton, etc., and is also useful in storage and transport of seeds to reduce premature germination which may affect agronomic or food quality of the seeds. The present sequence is soybean GA 2-oxidase 2 cDNA
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Pred. No. 5.6e-107;
0; Mismatches 327;
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al Similarity 66.0%;
669; Conservative
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This sequence represents cDNA encoding an Arabidopsis thaliana

gibberalin (GA) 2-oxidase, PcGA20x3. This enzyme is a GA 2-beta-

gibberalin (GA) 2-oxidase, pcGA20x3. This enzyme is a GA 2-beta-

CC gibberalin (GA) 2-oxidase, nc19-chs and for which 2-beta-hydroxylation is

is is only activity. Hydroxylation at the 2-beta position of a GA results

CC A metabolism in plants, ensuring that the active hormones do not

cacumulate in plant tissues. The nucleic acids can be used to transform

plants so that gibberalin 2-oxidase can be constitutively over-expressed

cor otherwise enhanced to reduce the concentration of bloactive GAs in the

plants and therefore to inhibit plant growth. Growth inhibition is useful

corpus and therefore and grain yield in cereals, improving seedling

cuality, reducing the growth of amenity grasses, reducing shoot growth in

corbard and ornamental trees, improving tolerance to cold, drought and

corbard and ornamental trees, improving tolerance to cold, drought and

corbard and increasing yields (by the diversion of assimilates from

vegetative to reproductive organs). The nucleic acids may also be used to

inflection, and increasing yields (by the will acrome and and increasing yields (by the context of acids may also be used to

inflection, expressioning, reduce shoot growth in commercial wood species. Antisense constructs of

reduce shoot growth in commercial wood species. Antisense constructs of

the nucleic acids can also be used to transform plants to reduce the
                                    1075
953 GGAGAGGAGTGTTTGTACAAAGAGTTCACATGGTGTGAATACAAGAAGGCTGCGTACACT 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated plant gibberellin 2-oxidase enzymes and nucleic acids, used to produce transgenic plants with improved or altered growth
                    1013 TCAAGGCTAGCTGATAATAGGCTTGCCCCTTTCCAGAAATCTGCTGCTGATTAA 1066
                                                                                                  1076 TCAAGATTGGCTGATAATAGGCTTGGACATTTTGAGAGAATTGTTGCTTCATAA 1129
                                                                                                                                                                                                                                                                                                                                                                          Gibberellin 2-oxidase; AtGA2ox3; 2-beta-hydroxylation; inactivation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "Gibberellin 2-oxidase AtGA2ox3"
                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana gibberellin 2-oxidase AtGA2ox3 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1. .1008
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phillips AL
                                                                                                                                                                                                                AAZSS917 standard; DNA; 1008 BP
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98GB-00015404
                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                              growth inhibition; ds.
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                                                                                                                                                                            RESULT 12
AAZ55917
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TGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAGCTGATAATAGGCTTGCCCCTTTC 1045
expression of GA 2-oxidase (claimed) to promote plant growth, (e.g., to improve fruit set and growth in seedless grapes, cirrus fruits and pears), improve skin texture and fruit shape in apples, increase stem length and therefore yield is sugar cane, increase yield and earliness in celery and rhubarb, improve malting yields and quality in cereals (particularly barley), and increase growth in woody species
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                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                         ;
                                                                                                                                                                  Score 382.8; DB 3; Length 1008; Pred. No. 2.2e-95;
                                                                                                                                Sequence 1008 BP; 296 A; 212 C; 232 G; 268 T; 0 U; 0 Other;
                                                                                                                                                                                                         0; Mismatches 327; Indels
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New isolated GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate synthase nucleic acid and proteins, useful for creating transgenic plants where polypeptides are present at higher or lower levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Orozco EM, Miao G, Famodu OO;
ai H, Weng Z, Caimi PG, Fang Y;
Shi J, Lu G, Helentjaris TG;
                                                                                                                                                   Wheat; ss; plant; plant metabolism; GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate synthase; Dioxygenase; Ent-Kaurene Synthase A; GA-20 oxidase; Gtbborellin 3-beta hydroxylase; Riboflavin specific deaminase; Ethylene response factor; Acyl-CoA thioseterase II; Palfycoproter GTOX Pellycoprotein I; P-glycoprotein 3; P-glycoprotein ATPGF; P-glycoprotein HVMNR2; ACG transporter; PMP70 ABC transporter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated polynucleotide comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                Rendina AR, Sakai H, Weng Z,
Anderson SL, Shi J, Lu G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; SEQ ID NO 7; 186pp; English.
1046 CAGAAATCTGCTGCTGATTAACCAAACA
                  973 GAGAAACGACCICCATTITCTCTATCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                     Rafalski JA,
                                                                                                                                                                                                                                                                                                                                                                                                        DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                  (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                               99US-0143401P.
99US-0143412P.
99US-0146650P.
99US-0170906P.
                                                                      ADM94207 standard; cDNA; 1473
                                                                                                                                                                                                                                                                                                            2000US-00614912
                                                                                                                                                                                                                                                                                                                                                                                     99US-0172959P
                                                                                                             (first entry)
                                                                                                                                 Wheat Dioxygenase cDNA #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Kinney AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Lohman KN, Re
Zoughi IL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-088430/09.
P-PSDB; ADM94208.
                                                                                                                                                                                                                                                Triticum aestivum.
                                                                                                                                                                                                                                                                   US6677502-B1
                                                                                                                                                                                                                                                                                                            12-JUL-2000;
                                                                                                             17-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                         21-DEC-1999;
21-DEC-1999;
                                                                                                                                                                                                                                                                                                                                 12-JUL-1999;
                                                                                                                                                                                                                                                                                         13-JAN-2004
                                                                                                                                                                                                                                                                                                                                            12-JUL-1999
                                                                                                                                                                                                                                                                                                                                                     30-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                15-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                Lee J, Lo
Shen JB,
Li CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Allen SM,
                                                                                                                                                                                                                                                                                                                                                                                                       ( DOLDO)
                                                           ADM9420
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                                                                               ò
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HVMDR2, ABC transporter, PMP70 ABC transporter and MRP4 ABC transporter.

The nucleic acid fragments may be used to create transgenic plants where the polymeptides are present at higher or lower levels than normal or in cell types or in developmental stages in which they are not normally cell types or in developmental stages in which they are not normally properties or in developmental stages in which they are not normally conditions. The polymucleotides can be used as probes for genetically and physically mapping genes and as markers for traits linked to those genes. The nucleic acid fragments may be used as restriction fragment length colymorphism (RFLP). It can also be used to probe Southern blots containing restriction endonuclease-treated genomic DNAs of a set of individuals representing parent and progeny of a defined genetic cross. The nucleic acid fragments may also be used as hybridisation probes against PCR amplification products generated from the mutation population using the mutation tag sequence primer in conjunction with an arbitrary genomic site primer. The peptides can also be used to immunise animals to produce polyclonal or monoclonal antibodies with specificity for peptides or produce polyclonal or monoclonal antibodies with specificity for peptides for detecting the polypeptides in altu in cells or in vitro in cell carrieds.
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Sequence 1473 BP; 285 A; 440 C; 468 G; 280 T; 0 U; 0 Other;

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299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 CCGACCCCGGGGACTACTTCTCCGGCATGCCGGTGGTCGACCTCTCCAGCCTTGGCGC 238
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                                                                                                                                                                                                                                                                                                        CAACAACCATGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAAACCAT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGCCATGGTGGTTCTCGCCAGCACGCCGCCGTCGATCACATCCCGCTCCTCAGGTCGC 178
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                                                                                                                                                                Gaps
        Length 1473;
                                                                                                                                                        6
                                                                                                                                                        0; Mismatches 374; Indels
Score 363.6; DB 12;
Pred. No. 5.6e-90;
27.6%;
al Similarity 61.3%;
607; Conservative
                                                                                Best Local Similarity
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780 CTTCCTTTTTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAA
                                                                                                                                                                                                      900 GAGGACCAGCGTTGAGTGAAATATAGCACCTTTACCTTCAGTGATGTTAAAAGGAGAGG
                                                                                                                                                                                                                                                                                                                                                         1010 AGAGCCTGTACAAGGACTTCACATGGGGGGGGTACAAGAAGGCTGCCTACAACTCCAGGC
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19-MAY-1999;
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Sequence 1316 BP; 440 A; 249 C; 252 G; 375 T; 0 U; 0 Other;
                                                                                            AAZ55915 standard; cDNA; 1316 BP
                                               RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219 TAGTCTCTGTTTTAGAACACGAGACGGTCGATTTCTTCTCGTTGCCCAAGTCAGAGAAA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   279 CCCAAGTCG---CAGGTTATCCCTTAGGATACGGGAACAGTAAGATTGGTCGGAATGGTG
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                                                                                                                                                                                            Gaps
                                                                                                                                                                                            12;
                                                                                                                                            Length 1224;
                                                                                                                                                                                            Indels
                                                                                                                                          Score 356.6; DB 3;
Pred. No. 4.5e-88;
0; Mismatches 329;
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99US-0161361P.
99US-0161920P.
99US-0161992P.
99US-0161993P.
                                                                                                                                            Query Match
Best Local Similarity 63.2%;
Matches 586; Conservative
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
29-0CT-1999;
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This sequence represents cuts encoding an Arabidopsis in Allandopsis in Allandopsis in Allandopsis in Allandopsis in Allandopsis configuration of a GA results by droxylase that acts on C19-GAs and for which 2-beta-hydroxylation is the only activity. Hydroxylation at the 2-beta position of a GA results in a biologically inactive product, and is the most important route for GA metabolism in plants, ensuring that the active hormones do not accumulate in plant tissues. The nucleic acids can be used to transform plants so that gibberellin 2-oxidase can be constitutively over-expressed or otherwise enhanced to reduce the concentration of bioactive GABs in the plants and hortrucultural applications such as enhancing cor otherwise enhanced to reduce the concentration of bioactive GABs in the plants and therefore to inhibit plant growth inhibitation is useful cording and contamental trees, improving tolerance to cold, drought and cordinary and increasing yields (by the diversion of assimilates from cordinary and increasing yields (by the diversion of assimilates from vegetative to reproductive organs). The nucleic acids may also be used to induce male and/or female sterility (by expression in floral organs), prevent pre-harvest sprouting, reduce growth in hedging plants, inhibit reversibility in the development or germination of seeds and creduce shoot growth in commercial wood species. Antisense constructs of the nucleic acids can also be used to transform plants to reduce the expression of GA 2-oxidase (claimed) to promote plant growth, est, to ease, improve skin texture and fruit shape in apples, increase stem clangor, improve malting yields and quality in cereals increase growth in woody species (particularly barley), and increase growth in woody species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d plant gibberellin 2-oxidase enzymes and nucleic acids, used transgenic plants with improved or altered growth
                                                                                                                                                                       2-oxidase; AtGA2ox1; 2-beta-hydroxylation; inactivation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents cDNA encoding an Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                            /product= "Gibberellin 2-oxidase AtGA2ox1"
                                                                                                                                   Arabidopsis thaliana gibberellin 2-oxidase AtGA2oxl cDNA
                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phillips AL;
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                                                                                                                                                                                          growth inhibition, ss.
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15-JUL-1998;
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                                                                          CCGGGTTCTCTCTATATTAGATATGTCTGACCCAGAATCCAAACATGCCTCG 137
                                                                                                         TGAACGCCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCCATTGGAGT 251
                                                                                                                                                              TAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAGAAAG 311
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                                                                                                                                                                                                                                     CCCAAGTCG---CAGGTTATCCCTTCGGATACGGGAACAGTAAGATTGGTCGGAATGGTG
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Ouery Match 27.1%; Score 356.6; DB 3; Length 1316; Best Local Similarity 63.2%; Pred. No. 4.6e-88; Matches 586; Conservative 0; Mismatches 329; Indels 12;
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Result

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Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla B., Marra, M., Hiller, L., Kucaba, T., Martin, J., Kanna, A., Bolla B., Marra, M., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., McCann, K., Waterston, R. and Wilson, R., Garkson, Y., Cardenas, M., McCann, K., Waterston, R. and Wilson, R.

In Unpublished (1999)
Other Estr: Buseaker R.Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
Washington University School of Medicine
H444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW184969 653 bp mRNA linear EST 24-JUL-2004 se84f09.yl Gm-c1023 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1023-1410 5' similar to TR:004162 004162 DIOXYGENASE. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: estGwatson.wustl.edu
When it has been determined, an EST from the other end of this clone is slated in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com) Insert Length: 1472 Std Error: 0.00
                                                                            CV292717 ESTRB1094
B1968577 GM330005B
BW685035 BW685035
CA844444 EA27D12a
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CV470333 EA26013a
CV459374 41999.1 C
DN501878 V035D04.5
BQ44995 GA EG007
BQ744995 GA EG007
BG744995 GA EG007
BG744995 GA EG007
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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/mol_type="mRNA"
/mol_type="mRNA"
/culfivar="T157"
/db xref="texton:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1023-1410"
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                       GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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1 (bases 1 to 566)
Shoemaker, R., Kein, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowert, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, B., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800

Fax: 314 286 1810

Bmail: estewatson.wustl.edu

Bmail: estewatson.wustl.edu

When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)

High quality sequence stopp: 426.

Location/Qualifiers
                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Pabales; Pabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                      Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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/organism="Glycine max"
/organism="Glycine max"
/mol_type="maxNa"
/cultivar="williams"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1066-4957"
/tissue type="Leaf and shoot tip, salt stressed, 2 void seedling"
                                                                                                                                                                                                                                                                                                                    Public Soybean EST Project
Unpublished (1999)
Glycine max (soybean)
Glycine max
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                       ORGANISM
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AUTHORS
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                                 /clone lib="Gm-c1023"
//note="Vector: pSPORT1; Site_1: Sal1; Site_2: NotI; This cDNA library was constructed from mRNA isolated from seed coats (100-200mgs) of greenhouse grown plants. The library was prepared using the Life Technologies pSuperScript cDNA library construction kit. Complimentary DNA was synthesized from mRNA using a poly (41) sequence with a Not I restrictions site. Sal I linkers adapers were ligated to the blunt-ended cDNA fragments followed by Not I digestion. The cDNA fragments were directionally cloned into the Not I sal I restriction site of the pSPORT1 vector. The ligated cDNA fragments were transformed into E.coli Electromax DH10B host cells. This library was constructed by Dr. Lila Vodkin and Dr. Anu Khanna."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 CCCACGCCCTTGTTCGCGGGGGATTCCTGTGGTCGACCTCACGGACCCCGATGCCAAGACC 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245 TIGGAGTTAATGGCCAATTTAGAAAACGAGGCCTCAGGTTCTTTAAAAAATCTCAGTCC 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 TTACAGTTCATGGCCAATTTGGAAAACGAAACCCTCGGGTTCTTCAAAAAACCTCAATCC 320
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'tissue_type="seed coats of greenhouse grown plants"
'lab_host="DH10B"
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Best Local Similarity 87.2%;
Matches 499; Conservative
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    Length 566;
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Score 444.8; DB 3;
Pred. No. 5e-108;
0; Mismatches 67;
  Query Match
Best Local Similarity 87.9%;
Matches 485; Conservative
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BMO85298 556 bp mRNA linear EST 23-JUL-2004 saj34h07.y1 Gm-c1066 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1066-4957 5' similar to TR:Q9XG83 Q9XG83 GA 2-OXIDASE. ;, mRNA

GI:16995926

sequence. BM085298 BM085298.1 EST.

ACCESSION VERSION KEYWORDS

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AAAGAGTTCACATGGTGTAATACAAGAAGGCTGCGTACATTCAAGGCTAGCTGATAAT 1030
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84.1%; Pred. No. 4.9e-104;
ive 0; Mismatches 88;
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/ Organism="Glycine max"

//mol_type="mkNa"

/db_xrefe="mkNa"

/clone="gm_r1089-5828"

/clone="gm_r1089-5828"

/clone="lgm_r1089-5828"

/note="The library Gm_r1088 is a sequence-driven, reracked

set of 9,216 low redundancy clones selected from cDNA

libraries from various tissues and stages of development

of soybean that consists of 2,706 cDNAs from germinating

cotyledons (source library Gm-c1027); 1,155 cDNAS from
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GM880016A20B10 Gm-r1088 Glycine max cDNA clone Gm-r1088-5828 3',
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                                                                                                                                                                                                        CCCAAATCACTTTGCATTTTCCGAGAAAATCCTCATCATTTCAGGGCGGTGGTGGAGAAC 484
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TTAGAGTICATGGCCAATTIGGAAAACGAAACCCICAGGTICTTCAAAAAACCTCAGTCC 254
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Tel: (217) 244-6147
Fax: (217) 333-4582
                                                                                                                                              AACGGCGATGTCGGTTGGGTCGAATACCTCCTTCTCAACACCCCAACCCTGACGTCATCTCC
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                                        GAGAAAGACAGAGCTGGTCCCCCCGACCCTTTCGGCTATGGTAGCAAGAGGATTGGCCCCA
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Other ESTS: BG881784 corresponding to Gm-c1065-2970 (5')
Contact: Vodkin, L.O., Pl, A Functional Genomics Program for Soybean (NSF 9872565)
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Insert Length: 622 Std Error: 0.00
Plate: GM880016A20 row: B column: 10
egg primer: 5'-TTTTTTTTTTTTTTTTTTTT (A/C/G)-3'
High quality sequence stop: 622.
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AUTHORS
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immature seed coats (libraries Gm-c1019 and Gm-c1023); 917 cDNAs from tissue culture derived somatic embryos (source libraries Gm-c1056, and Gm-c1056, cDNAs from germinating seedlings, shoot tips, or leaves exposed to various stresses (source libraries Gm-c1066, and Gm-c1067, and Gm-c1064, Gm-c1065, Gm-c1066, and Gm-c1067, and Gm-c1073, and span by the close from the dungal pathogens (source libraries Gm-c1072, Gm-c1073, and Gm-c1074). The Source clones from the different libraries was used to select singletons, or a representative of each contig, which were reacked to form library Gm-r1088 and the CDNA clones of the reracked Gm-r1088 library were then sequencing was funded by NSF Plant Genome project #9872565 (http://soybeangenomics.cropsoi.uiu.edu/) as part of creation of a low redundancy soybean cDNA set. The source CDNA libraries were constructed by the laboratories of Lila Vodkin, University, and Paul Kelim, Northern Arizona University, and Paul Kelim, Northern Arizona University, and Paul Kelim, Northern Arizona University as part of the Public EST project, the set Retzel, Center for Computational Genomics and Bioinformatics, University of Minnesota, sequencing were conducted by services of the University of Ernest Retzel, Center for Computational Genomics and Bioinformatics, University of Minnesota, sequencing were conducted by services of the University of Engented Marie EST from each clone can also information on the source library for each clone can also be obtained by referring to the Genome Systems clone ID of the Ormarial CDNA library that is also listed under 'OTHER EST'.

88; Indels 11; Gaps

613 562

670 502 730

442 382 850

AGGGTTTTGGCTGACAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACCAGCG

910

322

970

201 AAAGAATTCACATGGTGGGAATACAAGAAGGCTGCGTATGCGTCAAGGCTAGCGGATAAT

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TGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAGCTGATAATAGGCTTGCCCCTTTC 1045
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                                            GACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCCATTGGAGTTAATGGCCAATTTA
                                                                                                                                                              GAAAACGAGGCCCTCAGGTTCTTTAAAAATCTCAGTCCGAGAAAGACAGAGCTGGTCCC
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BX816963.
BX816963.1 GI:42471779
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The sequences are based on single pass reads
Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G. Genoscope embers carried out sequencing and annotation : Castelli V., Aury J.M., Jailno O., Wincker P., Menard M., Cruaud C., Cabachter V., Weissenbach J., Salanoubat M. Will Will Schachter V., Weissenbach J., Salanoubat M. Graud C., Caboche M. Salanoubat M. Salanoubat M. Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap. http://www.genoscope.cns.fr/externe/sequences/Banque_Er/Full length
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Castelli, V. Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,
Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
Whole Genome Sequence Comparisons and 'Pull-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                              HTC 06-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTFB7ZE01 of Flowers and buds of strain col-0 of Arabidopsis thaliana (thale cress).
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                                         82
http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
Location/Qualifiers
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/db_xref="taxon:3702"
/clone="GSLTFB7ZE01"
/tissue_type="Flowers and
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Submitted (18-NOY-2003) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr - The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G. Genoscope members carried out sequencing and annotation: Castelli Cv., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
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Arabidopsis thaliana (thale cress)
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; crosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
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The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGV INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
                                                                                                   Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weisenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
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[ [bases 1 to 1362]
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Location/Qualifiers
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ecotype="Col-0"
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Pred. No. 7.8e-103;
0; Mismatches 317;
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/db_xref="taxon:3702"
/clone="GSLTPGH78ZH09"
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases 1 to 1363)
Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
Menard,M., Craud,C., Quetler,F., Scarpelli,C., Schacher,V.,
Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
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Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :

BP 191 91006 EWRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G.

Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGV INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTPGH202C07 of Hormone Treated Callus of strain col-0 of Arabidopsis thaliana (thale cress).
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http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="GSLTPGH20ZC07"
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                      Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap. http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full_length
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/tissue_type="Flowers and
       URGV INRA : Clepet C., Caboche M.
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Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length librairies construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGY INRA : Clopet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences) : 5 prime and 3 prime are assembled with Phrap.
                                                                  Sukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons; rosids; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 1339)

Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C., Menard,M., Cruaud,C., Quetider,P., Scarpelli,C., Schachter,V., Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
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Location/Qualifiers
 BX814383.1 GI:42472054
HTC; GSLT. CDNA.
Arabidopsis thaliana (thale cress)
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1. .1339 /organism="Arabidopsis thaliana"

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                                                                                                                                                                        Length 1339;
                                                                                                                                                                                                         Indels
                                                                                                                                                                        Score 386.4; DB 4;
Pred. No. 3e-92;
0; Mismatches 281;
/mol_type="mRNA"
/db xrefe="taxon:3702"
/clone="GSLTFB702F11"
/tissue_type="Flowers and bu
/ecotype="Col-0"
                                                                                      'plasmid="pCMVSPORT_6"
                                                                                                                      /gene="At1g30040"
                                                                                                                                                                      tch 29.3%;
al Similarity 66.9%;
581; Conservative
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CNSOAC3R

Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTFBP0ZF11 of Flowers and buds of strain col-0 of Arabidopsis Exaliana (thale cress).

DEFINITION

FOCUS

RESULT 8 CNSOAC3R

ACCESSION

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/ Organism="Circula"
/ Organism="Circula"
/ Culfivar="Corolla"
/ Culfivar="Corolla"
/ Culfivar="Corolla"
/ Culfivar="Corolla"
/ Clone="GENOME SYSTEMS CLONE ID: Gm-c1051-1097"
/ Lissue_Type="floral meristematic mRNA"
/ Lissue_Type="floral meristematic mRNA provided by Dr. Hailna Knap of Clemson
/ Miversity. Complementary NDA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
XhoI restriction site. ECORI adapters were ligated to the
blunt-ended cDNA fragments followed by XhoI digestion. The
CDNA fragments were directionally cloned into the
ECORI-XhoI restriction site of the pBluescript vector. The
ligated cDNA fragments were transformed into blut bost
cells (GibcobRL). This library was constructed in the
laboratory of Dr. Randy Shoemaker."
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57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 28.7%; Score 378.6; DB 2;
Best Local Similarity 88.4%; Pred. No. 3.2e-90;
Matches 411; Conservative 0; Mismatches 54;
                                                                                                            'organism="Glycine max"
                            High quality sequence stop: 413.
Location/Qualifiers
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Antirrhinum majus
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Public Soybean EST Project
Washington University School of Medicine
Washington University School of Medicine
Washington University School of Medicine
Path Forset Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
When it est@watson.wustl.edu
When it has been determined, an EST from the other end of this
When it has been determined, an clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              612 bp mRNA linear EST 13-JUL-2004 Br46c09.yl Gm-c1051 Glycine max cDNA clone GENCME SYSTEMS CLONE ID: Gm-c1051-1097 5' similar to TR:O64692 O64692 PUTATIVE GA4 PROTEIN.
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Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Schurk, R., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
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CGTCAAACCCCTCAAATTTTCCGTGAGTCGAGGAGTACATGAAGGAGATTAAGGAA 552
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                                                      ATGTGCTATGCGGTGTTGGAATTGATGGCGGAGGGGTTGGGGATAAGGCAGAGGAATACG
                                                                                                            553 GTGTCGTACAAGGTGTTGGAGATGGTTGCCGAAGAACTAGGGATAGAGCCAAGGGACACT
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When you have constructed the sequence of the sequences are based on single pass reads.

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.

Genoscope members carried out sequencing and annotation: Castelli V., Aury J. W., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGV INRA: Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fi/externe/sequences/Banque_Projet_EF/Full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 1128)
Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,
Menard, M., Craud, C., Quetler, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                                                                                                                                                                               linear HTC 06-FEB-2004
                          TGTTTGTACAAAGAGTTCACATGGTGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTA 1021
                                                     677 AGCTTGTACAAGGAATTTACTTGGTTTGAGTACAAAAAATCTGCTTATAATCAAGGCTGG 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTC; GSLT_CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                          from clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192 TGAACGCCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCCATTGGAGT 251
                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana Full-length cDNA Complete sequence from clossITFB56ZG10 of Flowers and buds of strain col-0 of Arabidopsis thaliana (thale cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 CCTTGTTCACGGGGATTCCTGTGGTCGACCTCACGCACCCCGATGCCAAGAATCTCATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
Location/Qualifiers
1. .1128
/organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 ccesciricicrerariccesirarasarargrerereacceasaricaaacareceres
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                                                                                                                                                                                                                                                                                                               mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tissue type="Flowers and |
/ecotype="Col-0"
/plasmid="pCMVSPORT_6"
                                                                                                                                                                                                                                                                                                             1128 bp
                                                                                                                              1022 GCTGATAATAGGCTTGCCCCTTT 1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:3702"
/clone="GSLTFB56ZG10"
                                                                                                                                                                                 759
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                                                                                                                                                                              737 GCTGATAATAGGTGGGTCTGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                           BX814091.1 GI:42474058
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2 (bases 1 to 1128)
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Direct Submission
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Matches
                                                                                                                                                                                                                                                                                                                                     DEFINITION
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VERSION
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SOURCE
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AUTHORS
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CNSOADMT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTTTCAGGCTAAATCACTATCCACCATGCCCCGAATTTCAAGAATCCAAC---AACTTA 376
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, asterids, lamiids, Lamiales, Plantaginaceae, Antirrhineae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAAACGGTGATGTCGGTTGGGTCGAATACCTCCTCAACACCAACCCTGATGTTATC 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 TACAGAAAATTTGCATCGGTTTTTGGTGAAGCTGCAGAAAAATTCAGGTGTATAGTGAAT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      482 AACTACATTACAGCAGTGAAGAACATGTGCCTATGCGGTGTTGGAATTGATGGCGGAGGGG 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200 GATTATGTTTCTGCAGTAAGAGAATGGCGTGTGAGATTCTTGAAATGTTGGTGATGAA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTGGGGATAAGGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAGTGATTCG 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTGGGTTTGGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTAACAGCACA 721
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                                                                                                1 (bases 1 to 785)
Bey,M., Stueber,K., Fellenberg,K., Schwarz-Sommer,Z., Sommer,H.
Saedler,H. and Zachgo,S.
Characterization of Antirrhinum Petal Development and
Identification of Target Genes of the Class B MADS Box Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         377 ATCGGGTTTGGTGAACATACTGACCCGCAAATAATATTCGTTTTGAGATCCAACAACACT
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Pred. No. 4.5e-84;
0; Mismatches 232; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .785

/organism="Antirrhinum majus"

/mol type="mRNA"

/db xref="taxon:4151"

/clone="018 5 05 018"

/tissue type="whole plant"

/clone_lib="Antirrhinum majus whole plant"
                                                                                                                                                                                                                                                                       Contact: Schwarz-Sommer Z
Contact: Schwarz-Sommer Z
Molekulare Pflanzengenetik
MPI fuer Zuechtungsforschung
Carl-von-Linne Weg 10, D-50829, Germany.
Location/Qualifiers
                                                                                                                                                                                                                                                            Plant Cell 16 (12), 3197-3215 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
27.0%;
Best Local Similarity 68.4%;
Matches 508; Conservative
                                                                                Antirrhinum.
                                                                                                                                                                                                                                 DEFICIENS
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Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khama, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptcoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
McCan, K., Waterston, R., Swaller, T., Jackson, Y., Cardenas, M.,
McCan, R., Waterston, R., and Wilson, R.,
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Seq primer: -40RP from Gibco
High quality sequence stop: 435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Glone lib="Gm-cl069"
//Glone lib="Gm-cl069"
//note="Vector: pBluescript II SK+; Site I: EcoRI; Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
from degenerating cotyledons of 9-10 day old etiolated
seedlings for the cultivar Williams. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI xhoI restriction site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 TCCACGCCCTTGTTCACGGGGATTCCTGTGGTCGACCTCACGCACCCCCGATGCCAAGAAT 184
     cosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the pBluescript vector. The ligated cDNA fragments were transformed into DH108 host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214 CCCACGCCCCTGTTCTCCGGGATTCCCGTGGTCGACCTCACGACCCCCGATGCCAAGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCATGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAAACCATTCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274 CACATAGTGAAGGCCTGCAGGGACTTCGCTTCTTCAAGCTCGTGAACCACGGTGTTTCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue type="Degenerating cotyledons, 9-10 day etiolated seedling"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 567;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1069-2961"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 336.2; DB 3;
Pred. No. 7.7e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Glycine max"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/cultivar="Williams"
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al Similarity 88.4%;
365; Conservative
                                                           (bases 1 to 567)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       963 GTTTGTACAAAGAGTTCACATGGTGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAG 1022
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TGAAAGCATGCGAAGACTTCGGCTTCTTCAAGGTGATCAACCATGGCGTTTCGGCAGAGC 203
                                                                                                                                                  263
                                                                                                                                                                                                           371
                                                                                                                                                                                                                                                                 264 CCCAAGTCG---CAGGTTATCCCTTCGGATACGGGAACAGTAAGATTGGTCGGAATGGTG
                                                                                                                                                                                                                                                                                                                            431
                                                                                                                                                                                                                                                                                                                                                                               321 ACGTGGGTTGGGTTGAGTACTTGTTGATGAACGCTAATCATGATTCCGGTTCGGGTCCAC 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      441 CATCAGTGAGAAAAATGACATTCGATGTTTTGGAGAAGATCACAGATGGGCTAGGGATCA 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACCGAGGAACACACTIAGCAAGCTIGTATCTGACCAAAACACGGACTCGATATTGAGAC 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGAACCACTACCCGCCTTGCCCTGAGGTGCAAGCACTGAAC-----CGGAATTTGG 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGGGTTTGGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTAACAGCACAT 722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 741 CCTTCTTCTTCAACGTTGGTGACTCTCTCCAGGTGATGACAAATGGGAGGTTCAAGAGCG 800
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                                                                                            TAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAGAAAG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTGATGCCGGAGGGGTTGGGGATAA 551
                                                                                                                                                                                                                                                                                                                            ATGTCGGTTGGGTCGAATACCTCCTCAACACACCCAGGTGGTTATCTCACCCAAAT
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                                                                                                                                                  204 TAGTCTCTGTTTTAGAACACGAGAACGTCGATTTCTTCTCGTTGCCCAGGTCAGAAAAA
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/db_xref="taxon:3880"
/clone="MtBC10802"
/tissue_type="arbuscular mycorrhiza"
/dev_atage="harvested 3 weeks post inoculation with Glomus
intraradices"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL382874 478 bp mRNA linear EST 03-AUG-2000
MEBC10E02F1 MLBC Medicago truncatula CDNA clone MtBC10E02 T3, mRNA
                                         241 TATTGATGGATGAAAGAGCGACTCTGTTTCAGGCTGAATCACTATCCTCCATGTCCTG 300
                                                                                                                                          301 ATATTCAAGAATTCAATGCCAAAATTTAATTGGATTTGGAGAACATACTGATCCACAAA 360
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                                                                                                                                                                                                          CTTGGGTTTCAGTCCCACCTGATCAGACTTCCTTTTTCATCAATGTTGGTGACGCTCTAC 812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGTCAAGGTTATCAATGATCTACTTTGGAGGACCAGCGTTGAGTGAAAATATAGCACCTT 932
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Contact : Pascal Games and Etienne-Pascal Journet, Laboratcire of
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 27 3138 Castanet-Tolosan Cedex, France (Email: Mt-estétoulouse.inra.fr Website :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tobases 1 to 478)

Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O., Niebel, A., Carreau, V., Chatagnier, O., Kahn, D., Gianinazi-Pearson, V. and Gamas, P. Medicago truncatula ESTs from endomycorrhizal roots Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCTGAAGGATGAGAAAAGTGATTCGTGCTTCAGGTTGAACCACTACCCGCCTTGCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                        AGGTGCAAGCACTGAA - - - CCGGAATTTGGTTTGGGGAGCACACAGACCCACAGA
                                                                                                                                                                                           TAATTTCTGTCTTAAGATCTAACAGCACATCTGGCTTGCAAATCTGTCTCACAGATGGCA
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              993 ACAAGAAGGCTGCGTACACTTCAAGGCTAGCTGATAA 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Medicago truncatula"
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/cultivar="Jemalong"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="cTOS"
/note="Vector: pBluescript SK(-); Site 1: BCORI; Site 2:
Xho1; Suspension cultures of L.esculentum E6203 were grown
in Murashige and Skoog based medium, supplemented with 15%
coconut milk (filter sterilized and added after
autoclaving), 2% saccharose, and img/ml 2, 40 (pH5.8).
Presh medium was added every 7 days, and cultures were
grown at 25 C, with 12hrs of light and continuous
                                                                                                                                                                                                                                                                                          BI208568 50S Lycopersicon esculentum cDNA clone cTOS17020 5' end,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Lycopersicon esculentum (Solanum lycopersicum)
Lycopersicon esculentum
Lycopersicon esculentum
Lycopersicon esculentum
Lycopersicon esculentum
Lycopersicon esculentum
Sparmatophyta; Publiphyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamida; Solanales; Solanaceae; Solanum; Lycopersicon.
Labases 1 to 694)
Labases 1 to 694)
Ronning.C. and Tanksley,S.
Generation of ESTs from Tomato Suspension Cultures
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        455
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                       336 TCGGCTATGGTAGCAAGAGGATTGGCCCAAACGGTGATGTCGGTTGGGTCGAATACCTCC 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TCCTITCAACAATICIGAATICAATIACCAGAAATICGCAICTGTATIAGGIGICAATC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 CAGAAAACATTCGGGCTGCGGTGAATGATTATGTGTCATCAGTGAAGAAAATGTCATGTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            516 CGGTGTTGGAATTGATGGCGGAGGGGTTGGGGATAAGGCAGAGAATACGTTAAGCAGGT 575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rrdgriardscaaraacaaaarcegacaaaaregceararcegrieggrieaaracarre 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        396 TCCTCAACACCAACCCTGATGTTATCTCACCCAAATCACTTTGCATTTTCCGAGAAATC
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                                                                                                                                             CCCAAATCACTTTGCATTTTCCGAGAAAATCCTCATCATTTCAGGGCGGTGGT 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: CUGI
Clemson University
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.4%; Score 335.4; DB 2; Length 694; 69.6%; Pred. No. 1.3e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 1.3e-78;
0; Mismatches 206; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .694 // Crganism="Lycopersicon esculentum" // Organism="Lycopersicon esculentum" // Mol. Lype="nANA" // ES 203" // Cdb xref="taxon:4081" // Clone="cTOS17020"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="suspension cultures"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                              BI208568.1 GI:14686292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           485; Conservative
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                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
BI208568
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VERSION
KEYWORDS
SOURCE
ORGANISM
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JOURNAL
COMMENT
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BI208568
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/done liberLate Blight-Challenged Tubers"
/done liberLate Blight-Challenged Tubers
/note="Vector: pBluescript II SK(+) XR; Site 1: EcoRI;
Site 2: Xhoi; supplier: Pathogen-challenge series. Tubers
from pathogen-free Solanum tuberosum var. Shepody, clone
1756, were inoculated with 5 ul of Phytophthora infestans
(A2-mating type), through 2 puncture wounds 3 cm apart.
The tubers were inocubated 1 minute to allow inoculum
absorption. The infection area was outlined for future
collection reference. Surface splices were sampled from the
tubers at 1 day, 5 days, 7 days, 11 days and 14 days
post-infection All samples were pooled and used for RNA
isolation and library construction. A normalized library
was constructed following a modified protocol of Bonaldo
et al. (1996. Genome Research 6: 791-806)."
Koeyer, D., Audy, P., Goyer, C., Li, X.-Q., Wang-Pruski, G. and Regan, S. Generation of ESTB from late blight-challenged potato tubers Unpublished (2005)
Contact: Barry Flinn
The Canadian Potato Genome Project - BioAtlantech
Barry Flinn Petato Genome Project - BioAtlantech
Email: bflinn@bioatlantech.nb.ca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 329 GACCCTTTCGGCTATGGTAGCAAGAGGATTGGCCCAAACGGTGATGTCGGTTGGGTCGAA 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 AGTAAGCITTTAATGGATGAAAAAGTGATTCACTTTTTAGGCTAAATCATTACCCTCCA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                389 TACCICCICCAACACCCIGAIGITAICICACCCAAAICACTIIGCAITITCCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 TACATTCTTTTGTCAACAATTCTGAGTTCAATTACCAAAAATTTGCATCTATTTTGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   449 GAAAATCCTCATCATTTCAGGGCGGTGGTGGAGAACTACATTACAGCAGTGAAGAACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 GTCAATCCAAAAGATATAAGAGATGCTGTGAATGATTATGTATTAGCAATGAAGAAAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 GCTTGTGAGATTCTTGAAATGTTAGCAGAGGGATTAAAAATTCATCCAAAGAATGTATTT
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                                                                                                                                                                                                                                                                                                                        /organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Shepody"
                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:4113"
/clone="50141"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="Tubers"
/lab_host="XL10-Gold"
                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                            TITLE
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                  /note="Vector: pBluescript pSK; Site 1: ECORI; Site 2: Xho1; M. truncatula sterilised seeds were germinated for 72h at 25 C, before transplanting into a 1/3 Epoisses soil: 2/3 calcined Terragreen mix in the presence of onion root fragments colonized by the arbuscular mycorrhizal fungus Glomus intraradices (Schenck & Smith, isolate LPA8). The plants were watered every day and twice a week with a modified nutrient Long Ashton solution without phosphate but with a high level of nitrate. After 3 weeks RNA was extracted from whole root systems. CDNA was prepared from poly4+ enriched RNA. The cDNA was prepared from poly4+ enriched RNA. The cDNA was prepared from poly4+ enriched RNA. The cDNA was preased from poly4+ enriched RNA inserts were stracts. Plasmids containing cDNA inserts were mass-excised from plage stocks using EXAssit helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, Evry, France). Note: EST may be of fungal origin."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, asterids, lamids, Solanales, Solanaceae, Solanum.

1 (bases 1 to 893)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   728 TIGCAAATCTGTCTCACAGATGGCACTTGGGTTTCAGTCCCCCGGATCAGACTTCCTTT 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATAGGGTTTTGGCTGACACAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACCA 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATAGGGTTTTGGCTGACACAACAAGTCAAGGTTGTCGATGATATACTTTGGAGGACCA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               908 GCGTTGAGTGAAAATATAGCACCTTTACCTTCAGTGATGTTAAAAGGAGAGGAGTGTTTG 967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        968 TACAAAGAGTTCACATGGTGTGAATACAAGAGGCTGCGTACACTTCAAGGCTAGC 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                557 AGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAAGTGATTCGTGCTTCAGGTTGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
25.3%; Score 332.8; DB 1; Length 478;
Best Local Similarity 83.0%; Pred. No. 6.1e-78;
Matches 395; Conservative 0; Mismatches 72; Indels 9
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        543 AATAGTGTAAAATCAAGACTCTCAATGATTTATTTGGAGGGCCACCATTGAGTGAAAAG 602

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December 27, 2005, 17:48:03; Search time 268.271 Seconds (without alignments) 8733.074 Million cell updates/sec
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Description	Sequence 1, Appli Sequence 13, Appli Sequence 13, Appli Sequence 7, Appli Sequence 4, Appli Sequence 7, Appli Sequence 7, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 66, Appli Sequence 66, Appli Sequence 66, Appli Sequence 68, Appli Sequence 10, Appli Sequence 10, Appli Sequence 11, Appli Sequence 12, Appli Sequence 13, Appli Sequence 14, Appli Sequence 16, Appli Sequence 17, Appli Sequence 17, Appli Sequence 18, Appli Sequence 17, Appli
SUMMARIES	US-09-719-108-1 US-09-711-307-62 US-09-614-912-13 US-09-614-912-13 US-09-719-108-7 US-09-719-108-7 US-09-719-108-7 US-09-614-912-7 US-09-614-912-1 US-09-614-912-1 US-09-614-912-1 US-09-711-307-68 US-09-371-307-68 US-09-371-307-68 US-09-371-307-68 US-09-371-307-68 US-09-371-307-68 US-09-371-307-68 US-09-371-307-68 US-09-371-307-68 US-09-371-307-68 US-09-371-307-68 US-09-371-307-68 US-09-371-307-68 US-09-371-307-68 US-09-371-307-68 US-09-371-307-58 US-09-719-108-3 US-09-719-108-3 US-09-719-108-3 US-09-719-108-3 US-09-719-108-3 US-09-719-108-3 US-09-719-108-3 US-09-719-108-3 US-09-719-108-3
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                                                      APPLICANT: Brown, Sherri M.
APPLICANT: Heck, Gregory R.
APPLICANT: Piller, Kenneth J.
APPLICANT: Elich, Tedd D.
APPLICANT: Loguech, Ragene W.
APPLICANT: Ganesh M.
APPLICANT: Baich, Tedd D.
APPLICANT: Back, Bool E.
APPLICANT: Ream, Joel E.
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APPLICANT: Methods for controlling gib PILE OF INVENTION: Methods for controlling gib FILE REFERENCE: MOBT:216
CURRENT FILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 62
LENGTH: 1359
TYPE: DNA
               Sequence 62, Application US/09371307A Patent No. 6723897 GENERAL INFORMATION:
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ŝ 124 158 218 244 278 304 338 364 339 GAGAAAGACAGGCTGGTCCCCTGACCCTTTTGGCTACGGCAGCAAGAGGAGTTGGCCCT 398 424 458 484 518 544 578 604 638 661 698 125 TCCACGCCCTTGTTCACGGGGATTCCTGTGGTCGACCTCACGCACCCCCGATGCCAAGAAT 184 ACCATGGTTGTTCTGTCTCAGCCAGCATTAAACCAGTTTTTCCTTCTGAAAACATGCAAG 219 CACATAGTCAATGCCTGCAGGACTTCGGCTTCTTCAAGCTCGTAAACCACGGTGTTCCG 279 TTACAGTTCATGGCCAATTTGGAAAACGAAACCCTCGGGTTCTTCAAAAAACCTCAATCC 399 AACGGCGATGTCGGTTGGGTCGAATACCTTCCTCAACACAACCCTGATGTCATCTCC 519 TACATTAGAGCGGTGAACAACATGTGCTATGAGGTGTTGGAATTGATGGCTGAGGGATTG 605 TICAGGITGAACCACIACCCGCCTIGCCCIGAGGIGCAAGCACIGAAC---CGGAAITIG 65 ACCATGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAAACCATTCAAG 159 CCCACGCCCTTGTTCGCGGGGATTCCTGTGGTCGACCTCACGGACCCCGATGCCAAGACC CTCATAGTGAACGCCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCCA TTGGAGTTAATGGCCAATTTAGAAAAGGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCC GAGAAAGACAGAGCTGGTCCCCCCGACCCTTTCGGCTATGGTAGCAAGAGGATTGGCCCA 365 AACGGTGATGTCGGTTGGGTCGAATACCTCCTCCAACACCCAACCCTGATGTTATCTCA 485 TACATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTGATGGCGGAGGGGTTG 545 GGGATAAGGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGATTCGTGC 31;

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445 414 505 474 553 534 613 594 673

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206 GAACTGCATGCCAACCAATTTTCCTCAACAATTCCCATAGTGGACCTCTCCAAACCTGA 265
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Pred. No. 1.2e-117;
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larity 65.7%;
Conservative
   Microsoft Office
; SOFTWARE: MicroBoft; SEQ ID NO 13
; LENGTH: 1352
; TYPE: DNA
; ORGANISM: Glycine m: US-09-614-912-13
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Matches 665
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 819 TCCTTTTTCATCAATGTTGGTGACACTCTTCAGGTAATGACTAATGGGGGGGTTTAAAAGT
                                                                                                                                                GTAAAGCATAGAGTTTTGGCTGACCCAACTCAAGGTTGTTGCATGATCATCTACTTTGGA
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                                                                   TCCTTTTTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGT
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APPLICANT: Rafalski, Antoni
APPLICANT: Orozco, Buddy
APPLICANT: Famcd, Gou-Hau
APPLICANT: Famcd, Gou-Hau
APPLICANT: Famcd, Gou-Hau
APPLICANT: Famcd, Hajime
APPLICANT: Sakai, Hajime
APPLICANT: Gaimi, Perry G
APPLICANT: Weng, Zude
APPLICANT: Anderson, Shawn
TITLE REFERENCE: Ball378 US NA
CURRENT APPLICATION NUMBER: US/09/614,912
CURRENT APPLICATION NUMBER: 60/143,401
PRIOR APPLICATION NUMBER: 60/143,401
PRIOR PILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/143,412
PRIOR PILING DATE: 1999-07-12
PRIOR PILING DATE: 1999-07-12
PRIOR PILING DATE: 1999-07-13
PRIOR PILING DATE: 1999-12-15
PRIOR PILING DATE: 1999-12-15
PRIOR PILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
PRIOR PILING DATE: 1999-12-11
PRIOR PILING DATE: 1999-12-21
PRIOR PILING DATE: 1999-12-21
PRIOR PILING DATE: 1999-12-21
PRIOR PILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 204
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Patent No. 6677502
GENERAL INFORMATION:
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Rafalski, Antoni
Orozco, Buddy
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                  415 TGTTATCTCACCCAAATCACTTTGCATTTTCCGAGAAAATCCTCATCATTTCAGGGCGGT 474
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                                                           513 ACACAACT-----TCTCTGTTTATGCCAAAAACCCTGAGAATTCAGGTGTCT
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                                                                                                      GGTGGAGAACTACATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTGATGGC
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Sequence 7, Application US/09719108
Patent No. 6670527
GENERAL INFORMATION:
APPLICANT: Thomas, Stephen G
APPLICANT: Hedden, Peter
TITLE OF INVENTION: Gibberellin 2-Oxidase
FILE REFRENCE: 0623.0970000
CURRENT PAPLICATION UNMBER: US/09/719,108
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: PCT/GB99/01857
PRIOR APPLICATION NUMBER: GB 9812821.8
PRIOR APPLICATION NUMBER: GB 9815404.0
PRIOR FILING DATE: 1998-06-11
PRIOR PRILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 16
SEQ TWARE: Patentin Ver: 2.1
SEQ ID NO 7
LENGTH: 1237
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US-09-719-108-7
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Pred. No. 3.7e-117;
0; Mismatches 333;
                                                                                                                                                                                                                                                                                                                    APPLICANT: Miao, Gou-Hau
APPLICANT: Famodu, Omolayo O.
APPLICANT: Eac, Jian Ming
APPLICANT: Sakai, Hajime
APPLICANT: Sakai, Hajime
APPLICANT: Sakai, Hajime
APPLICANT: Weng, Zude
APPLICANT: Weng, Zude
APPLICANT: Maderson, Shawn
TITLE OF INVENTION: Plant Metabolism Genes
FILE REFERENCE: BB1378 US NA
CURRENT APPLICATION NUMBER: US/09/614,912
CURRENT FILING DATE: 1999-07-12
PRIOR PILING DATE: 1999-07-12
PRIOR PILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/143,401
PRIOR APPLICATION NUMBER: 60/143,401
PRIOR PILING DATE: 1999-07-12
PRIOR PILING DATE: 1999-07-12
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: 60/172,956
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/172,946
PRIOR FILING DATE: 1999-12-21
                                                                                                                                                     RESULT 4
US-09-614-912-5
Sequence 5, Application US/09614912
; Patent No. 6677502
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ilarity 65.6%;
Conservative
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Rafalski, Antoni
Orozco, Buddy
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APPLICANT: Brown, Sherri M.
APPLICANT: Heck, Gregory R.
APPLICANT: Piller, Kenneth J.
APPLICANT: Piller, Kenneth J.
APPLICANT: Elich, Tedd D.
APPLICANT: Elich, Tedd D.
APPLICANT: Ream, Joel E.
APPLICANT: Ream, Joel E.
APPLICANT: Ream, Joel E.
APPLICANT: Logusch, Sherry J.
TILE REFERENCE: MOBT:216
TILE REFERENCE: MOBT:216
CURRENT PILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIN Ver. 2.0
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 64
LENGTH: 1403
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llarity 66.0%; Pred. No. 7.7e-116;
Conservative 0; Mismatches 327;
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CORGANISM: Glycine max
US-09-371-307-64
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                                                           ATTCCTGTGGTCGACCTCACGCACCCCGATGCCAAGAATCTCATAGTGAACGCCTGTAGG
                                                                                 GAATACCTCCTCCTCAACACCCAACCCTGATGTTATCTCACCCAAATCACTTTGCATTTTC
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                         3.
                         Indels
         Pred. No. 3.6e-116;
0; Mismatches 317;
         66.3%;
       Best Local Similarity 66.3
Matches 629; Conservative
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AACAGCACATCTGGCTTGCAAATCTGTCTCACAGATGGCACTTGGGTTTCAGTCCCACCT

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RESULT 6
US-09-371-307-64
Sequence 64, Application US/09371307A
Patent No. 6723897
GENERAL INFORMATION:

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TGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAGCTGATAATAGGCTTGCCCCTTTC 1045
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379 CGGCACACCCCTGCAATTTTCAGAGAGGCAGTGGAAGAGTACATTAAAGAGATAGAAGAGA 438
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                                           ATGTGCTATGCGGTGTTGGAATTGATGCCGGAGGGGTTGGGGGATAAGGCAGAGAATACG
                                                                                ATGTCGAGCAAATTCTGGAAATGGTAGAGGAAGAGCTAAAGATAGAGCCAAAGGAGAAG
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APPLICANT: Miao, GOU-Hau
APPLICANT: Famodu, Omolayo O.
APPLICANT: Sakai, Hajime
APPLICANT: Sakai, Hajime
APPLICANT: Sakai, Hajime
APPLICANT: Caimi, Perry G
APPLICANT: Caimi, Perry G
APPLICANT: Caimi, Perry G
APPLICANT: Anderson, Shawn
TILE OF INVENTION: Plant Metabolism Genes
FILE REFERENCE: BB1378 US NA
FILE REFERENCE: BB1378 US NA
FILE REFILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: 60/143,401
PRIOR APPLICATION NUMBER: 60/143,412
PRIOR PILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/146,650
PRIOR APPLICATION NUMBER: 60/170,906
PRIOR PILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: 60/170,906
PRIOR PELING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/170,906
PRIOR APPLICATION NUMBER: 60/170,906
PRIOR APPLICATION NUMBER: 60/170,906
PRIOR APPLICATION NUMBER: 60/170,906
PRIOR APPLICATION NUMBER: 60/172,959
PRIOR APPLICATION NUMBER: 60/172,959
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Patent No. 6677502
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Rafalski, Antoni
Orozco, Buddy
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                                         868
                                                                                  TITAAAAGIGTAAAGCATAGGGTTTTGGCTGACACAAGGAAGTCAAGGTTATCAATGATC 892
                                                                                                                      899 TITCGAAGIGIGAAACACAGAGTITITGACAAATGGATTTAAGTCTAGACTCTCAATGATT 958
                                                                                                                                                                  TACTTTGGAGGACCAGCGTTGAGTGAAAATATAGCACCTTTACCTTCAGTGATGTTAAAA 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 ATTCCTGTGGTCGACCTCACGCACCCCGATGCCAAGAATCTCATAGTGAACGCCTGTAGG 205
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                            GATCAGACTTCCTTTTTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGG
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Pred. No. 2.1e-103;
0; Mismatches 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/09719108
Patent No. 6670527
GENERAL INNORMATION:
GENERAL INNORMATION:
APPLICANT: Thomas, Stephen G
APPLICANT: Hedden, Peter
APPLICANT: Phillips, Andrew L
ITILE OF INVENTION: Gibberellin 2-Oxidase
FILE REFERENCE: 0623.097000
CURRENT APPLICATION NUMBER: US/09/719,108
CURRENT APPLICATION NUMBER: US/09/719,108
FILE REPEASION DATE: 1999-06-11
PRIOR APPLICATION NUMBER: GB 9812821.8
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 16
SSEQ ID NOS: 16
SSEQ ID NOS: 16
SSEQ ID NOS: 16
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; ORGANISM: Arabidopsis thaliana
US-09-719-108-9
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Best Local Similarity 64.1
Matches 595; Conservative
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LENGTH: 1008
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       960 AGTGTTTGTACAAAGAGTTCACATGGTGTGAATACAAGAAGGCTGCGTACACTTCAAGGC
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27.1%; Score 356.6; DB 3; Length
Best Local Similarity 63.2%; Pred. No. 1.5e-95;
Matches 586; Conservative 0; Mismatches 329; Indels
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APPLICANT: Hedden, Peter
APPLICANT: Hedden, Peter
APPLICANT: Phillips, Andrew L
APPLICANT: Hillips, Andrew L
APPLICANT: Phillips, Andrew L
CURRENT PLING SIDER: 05/0000
CURRENT APPLICATION NUMBER: US/09/719,108
CURRENT PLING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: GB 9812821.8
PRIOR PLING DATE: 1999-06-11
PRIOR PLING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTING DATE: 1998-07-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANIZM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
1.CCATION: (1243, 1265)
OTHER INFORMATION: unidentified residue
US-09-719-108-5
                                                                                                                                                                                                                                                                                                                                                   US-09-719-108-5; Sequence 5, Application US/09719108; Patent No. 6670527
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Pred. No. 1.4e-97;
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PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 204
SOFTWARE: Microsoft Office 97
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                  Query Match 27.6%;
Best Local Similarity 61.3%;
Matches 607; Conservative
                                                                                                                                                                             ; TYPE: DNA
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US-09-614-912-7
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APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Gaugla
APPLICANT: Famodu, Omolayo O.
APPLICANT: Famodu, Omolayo O.
APPLICANT: Famodu, Omolayo O.
APPLICANT: Gani, Petry
APPLICANT: Gani, Petry
APPLICANT: Gani, Petry
APPLICANT: Caimi, Petry
APPLICANT: Caimi, Petry
APPLICANT: Weng, Zude
APPLICANT: Nunderson, Shawn
TITLE OF INVENTION: Plant Metabolism Genes
FILE REFERENCE: BB1378 US/09/614,912
CURRENT FILING DATE: 1999-07-12
PRIOR PELICATION NUMBER: 60/143,401
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/170,906
PRIOR FILING DATE: 1999-12-15
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; ORGANISM: Oryza Bativa
US-09-614-912-3
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  Length 1650
                                             0; Mismatches 375; Indels
  Score 354; DB 3;
Pred. No. 1e-94;
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  26.9%;
Query Match
Best Local Similarity 60.99
Matches 598; Conservative
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APPLICANT: Heck, Gregory R.
APPLICANT: Filler, Kenneth J.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Logusch, Fugene W.
APPLICANT: Logusch, Sudabathula
APPLICANT: Rao, Sudabathula
APPLICANT: Rao, Sudabathula
APPLICANT: Logusch, Sherry J.
TITLE OF INVENTYON: Methods for controlling gibberellin levels
TILE OF INVENTYON: Methods for controlling gibberellin levels
TILE REFERENCE: MOST: 1999-08-10
CURRENT FILING DATE: 1999-08-10
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 4.4e-82;
0; Mismatches 170; Indels 18;
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GENERAL INFORMATION:
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Matches 441; Conservative
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ORGANISM: Gossypium hirsutum
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US-09-371-307-67
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US-09-371-307-67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 CCGGGCCCCAGGGACAGCTTCTCGGGAGTGCCGGTCGTCGACCTGTCCAGCCACCACGCGCG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTTCCATTGGAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAATCT 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Greececedecraterareacecedarecedadecereraderrerrecedadece 351
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Pred. No. 2.4e-83;
0; Mismatches 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Taint, Perry G
APPLICANT: Anderson, Shawn
TITLE OP INVENTION: Plant Metabolism Genes
FILE REFERENCE: BB1378 US NA
CURRENT APPLICATION NUMBER: US/09/614,912
CURRENT FILING DATE: 2000-07-12
PRIOR PAPLICATION NUMBER: 60/143,401
PRIOR PILING DATE: 1999-07-12
PRIOR PILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/146,650
PRIOR APPLICATION NUMBER: 60/146,650
PRIOR APPLICATION NUMBER: 60/170,906
PRIOR APPLICATION NUMBER: 60/170,906
PRIOR APPLICATION NUMBER: 60/170,959
PRIOR PILING DATE: 1999-12-15
PRIOR PILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 204
SOFTWARE: MICROSOFT OFFICE 97
                                                                                                  Sequence 1, Application US/09614912
Patent No. 6677502
GENERAL INFORMATION:
                                                                                                                                                                                                 Allen, Steve
Rafalski, Antoni
Orozco, Buddy
Miao, Gou-Hau
Famodu, Omolayo O.
Lee, Jian Ming
Sakai, Hajime
Weng, Zude
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Best Local Similarity 58.9%;
Matches 586; Conservative
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                                                               US-09-614-912-1
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Sequence 66, Application US/09371307A Patent No. 6723897
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NAME/KEY: unsure
LOCATION: (178)
CTHER INFORMATION: n = a,
US-09-371-307-66
Best Local Similarity
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ORGANISM: Glycine
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US-09-371-307-66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           412 GGTGACTCCTTACAGGTAATGACCAATGGAAGGTTTAAAAGGGTAAAAACATAGGGTAGTG 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                532 AAAATAGCACCTTTGCCATCTTTGATGAGGGGGATCAACAAAGCTTATATAAAGAATTT 591
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                                                                                                                        112 ATACTTGAAATGATGGCTGATGGGTTGAAGATACAACCCAGGAATGTGTTGAGCAAGCTG 171
                                                                                                                                                                                               172 TTGATGGATGAAGAGAGAGTCTCTTTTCAGGGTGAATCATTACCCCACCATGCCCTAAT 231
                  CATCATTTCAGGGCGGTGGTGGAGAACTACATTACAGCAGTGAAGAACATGTGCTATGCG
                                                                                        518 GTGTTGGAATTGATGGCGGAGGGGTTGGGGATAAGGCAGAGGAATACGTTAAGCAGGTTG
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APPLICANT: Brown, Sherri M.
APPLICANT: Piller, Kenneth J.
APPLICANT: Piller, Kenneth J.
APPLICANT: Elich, Tedd D.
APPLICANT: Logusch, Bugene W.
APPLICANT: Ream, Joel E.
APPLICANT: APPLICANT: MOBT: 216
CURRENT PILLE REFERENCE: MOBT: 216
CURRENT FILLNG DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 71
LENGTH: 811
LENGTH: 811
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US-09-371-307-71
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US-09-371-307-71
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965 ITGTACAAAGAGTTCACATGGTGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAGCT 1024
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APPLICANT: Brown, Sherri M.
APPLICANT: Brown, Sherri M.
APPLICANT: Heck, Gregory R.
APPLICANT: Filter, Kenneth J.
APPLICANT: Elich, Tedd D.
APPLICANT: Brown, Joel B.
APPLICANT: Ream, Joel B.
APPLICANT: Logusch, Sherry J.
TITLE OF INVENTION: Methods for controlling gibberellin levels
FILE REPREBENCE: MOBT:216
CURRENT FILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 66
LENGTH: 403
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al Similarity 55.8%; Pred. No. 7e-39;
316; Conservative 0; Mismatches 250; Indels
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                                                                    284 TICTITAAAAATCTCAGTCCGAGAAAGACAGAGCTGGTCCCCCCGGCCTTTCGGCTAT
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APPLICANT: Heck, Gregory R.
APPLICANT: Heck, Gregory R.
APPLICANT: Filler, Kenneth J.
APPLICANT: Kiehere, Ganesh M.
APPLICANT: Rich, Tedd D.
APPLICANT: Blich, Tedd D.
APPLICANT: Rao, Sudabathula
APPLICANT: Ream, Joel E.
APPLICANT: Ream, Joel E.
APPLICANT: Ream, Sudabathula
APPLICANT: Loqusch, Sherry J.
TITLE OF INVENTION: Methods for controlling gibberellin levels
FILE REFERENCE: MOBT:216
CURRENT APPLICATION NUMBER: US/09/371,307A
CURRENT FILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 68
LENGTH: 406
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   Length 403;
11.8%; Score 155.6; DB 3; Length 63.2%; Pred. No. 5.8e-36; ive 0; Mismatches 140; Indels
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LOCATION: (306)

CHER INFORMATION: n = a, c, US-09-371-307-68
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                   Best Local Similarity ...-
Matches 261; Conservative
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Matches 279; Conservative
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CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: US/09/19,108
RIOR PILING DATE: 2000-12-08
RIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: PCT/GB99/01857
PRIOR APPLICATION NUMBER: PG 9812821.8
PRIOR PILING DATE: 1999-06-11
PRIOR PILING DATE: 1998-06-12
PRIOR PILING DATE: 1998-07-15
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Sequence 67, Appl
Sequence 613, Ap
Sequence 141, App
Sequence 9278, Ap
Sequence 7861, Ap
Sequence 7861, Ap
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Sequence 62, Appl
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Sequence 1350, Ap
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Sequence 64, Appl
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Sequence 78659, A
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Sequence 3, Appli
                                                                                                                                         December 27, 2005, 17:51:22 ; Search time 1238.83 Seconds (without alignments) 8797.858 Million cell updates/sec
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100.0%; Score 1318; 100.0%; Pred. No. 0; ive 0; Mismatches

Query Match 100. Best Local Similarity 100. Matches 1318; Conservative

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TYPE: DNA ORGANISM: Phaseolus coccineus

9 9 240

181 GAATCTCATAGTGAACGCCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGT

CAAGTCCACGCCCTTGTTCACGGGGATTCCTGTGGTCGACCTCACGCACCCCGATGCCAA 180

AACAACCATGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAAACCATT 120

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1 GITICICTIACCCIGATCIGCTACTCTITITCATAGIAACAATCGACAACAACAAC

GTTTCTCTTCCTTACCCTGTTCTGCTTCTTTTTCATAGTAACAATCGACAACAACAAC

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25	188.6	_	1322	-	US-10-425-114-4257	Sednence	4257, Ap
26	188	14.3	1327	œ	US-10-425-115-103352	Seguence	103352,
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31	169.8		802	œ	US-10-425-115-177171	Sequence	177171,
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34	156.2		504	ø	US-10-259-194A-614	Sequence	. 🕶
35	155.6		403	m	US-09-371-307-66	Sequence	٠.
36	155.6		403	ø	US-10-401-321-66	Sequence	
37	154.8		406	m	US-09-371-307-68	Sequence	8
38	154.8		406	9	US-10-401-321-68	Sequence	
39	152.4		996	m	US-09-371-307-58	Sequence	
40	152.4	11.6	996	v	US-10-401-321-58	Sequence	58, Appl
C 41	150.4	11.4	537	9	US-10-259-194A-453	Sequence	453, App
4	146.4	11.1	322	~	US-10-424-599-67680	Sequence	67680, A
4.3	140 4	10.7	2478	-	US-10-437-963-20123	Sequence	20123. A
44	133.8	201	457		US-10-424-599-42166	Sequence	42166. A
4.5	127.4	0	797	. [IIS-10-424-599-108868	Seguence	108868.
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					ALIGNMENTS		
# H1000							
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Seque	ince 1,	Sequence 1, Application US/10670454	ion US/	.901	70454		
Publ:	cation	Publication No. US20040229357A1	0402293	57A.	-		
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APPI	ICANT:	APPLICANT: Thomas, Stephen	Stephen	Ø			
; APPI	APPLICANT:	Hedden, Peter	Peter				
, APPI	APPLICANT:	Phillip	Phillips, Andrew L	e¥			
IIII ;	E OF IN	VENTION:	Gibber	611	TITLE OF INVENTION: Gibberellin 2-Oxidase		
; FILE	REFEREI	FILE REFERENCE: 0623.0970000	3.09700	8			
, curi	ENT APP	LICATION	NUMBER	ë 	CURRENT APPLICATION NUMBER: US/10/670,454		
COR	KENT FIL	CURRENT FILING DATE:	: 2003-09-26	60-	-26		
Tan	T TOOK OF	MATTON N	TOVORD.	/ 511	DEPTOR ADDITION NUMBER: 118/09/719 108		

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Sequence 3, Application US/10821711

PUDIcation No. US20040237142A1

GENERAL INFORMATION.

APPLICANT: Gilberteon, Larry A

APPLICANT: Krieger, Elysia K

APPLICANT: Ye, Xudong

APPLICANT: Ye, Xudong

TITLE OF INVENTION: COMMERCIALLY VIABLE TRANSGENIC PLANTS

FILE REPERENCE: 38-21(52967)B

CURRENT PLING DATE: 2004-04-08

PRIOR APPLICATION NUMBER: 05/461,459

PRIOR FILING DATE: 2003-04-09

SEQ ID NO 3

LENGTH: 999
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al Similarity 100.0%; Pred. No. 2.1e-281;
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US-10-401-321-62
; Sequence 62, Application US/10401321
; Publication No. US20030233679A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
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                                                                      TTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTGTAAAG
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                      TTGCAAATCTGTCTCACAGATGGCACTTGGGTTTCAGTCCCACCTGATCAGACTTCCTTT
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   TTGCAAATCTGTCTCACAGATGGCACTTGGGTTTCAGTCCCACCTGATCAGACTTCCTTT
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US-09-371-307-62
US-09-371-307-62
i Sequence 62, Application US/09371307A
i Patent No. US20020053095A1
i GENERAL INFORMATION:
i APPLICANT Brown, Sherri M.
i APPLICANT Kishore, Ganesh M.
i APPLICANT Eller, Kenneth J.
i APPLICANT Eller, Kenneth J.
i APPLICANT Stance, Ganesh M.
i APPLICANT Rao, Sudabathula
i APPLICANT Rao, Usel E.
i APPLICANT RAOFILE STANT 
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                          819 TCCTTTTTCATCATGTTGGTGACACTCTTCAGGTAATGACTAATGGGAGGTTTAAAAGT
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                                                                                                   GTAAAGCATAGGGTTTTTGGCTGACACGAAGGTCAAGGTTATCAATGATCTTTGGA
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Publication No. US20040229357A1
GENERAL INPORMATION:
APPLICANT: Thomas, Stephen G
APPLICANT: Hedden, Peter
APPLICANT: Hillips, Andrew L
TITLE OF INVENTION: Gibberellin 2-Oxidase
CURRENT APPLICATION WUMBER: US/10/670,454
CURRENT FILING DATE: 2003-09-26
FRIOR APPLICATION NUMBER: US/09/719,108
FRIOR FILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: EPT/GB99/01857
PRIOR FILING DATE: 1999-06-11
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-13
PRIOR FILING DATE: 1998-06-15
PRIOR FILING DATE: 1998-07-15
SEQ ID NOS: 16
SEQ ID NO 7
SEQ ID NO 7
SEQ ID NO 7
SEQ ID NO 7
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          APPLICANT: Filler, Kenneth J.
APPLICANT: Kilbhore, Ganesh M.
APPLICANT: Elich, Tedd D.
APPLICANT: Blich, Tedd D.
APPLICANT: Ream, Usel B.
APPLICANT: Ream, Joel E.
APPLICANT: Ream, Joel E.
APPLICANT: Ream, Joel E.
APPLICANT: Baerson, Scott R.
TITLE OF INVENTION: Methods for Controlling Gibberellin Levels
TITLE OF INVENTION: Methods for Controlling Gibberellin Levels
CURRENT APPLICATION NUMBER: US/10/401,321
CURRENT APPLICATION NUMBER: US/10/401,321
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.2
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Pred. No. 1.7e-250;
1; Mismatches 158; Indels
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Best Local Similarity 84.9%;
Matches 1069; Conservative
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Pred. No. 2.8e-113;
0; Mismatches 306;
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
LENGTH: 1026
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1350
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Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Title OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
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          GACTICGGCTTCTTCAAGCTTGTGAACCATGGTGTTCCATTGGAGTTAATGGCCAATTTA
                                     GAGTTCGGGTTCTTCAAGGTCGTAAACCACGGAGTCCGACCCGAACTCATGACTCGGTTA
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US-09-938-842A-1350
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TGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAGCTGATAATAGGCTTGCCCCTTTC 1045
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                          CCACAGATAATTTCTGTCTTAAGATCTAACAGCACATCTGGCTTGCAAATCTGTCTCACA
                                                                                                                                                          571 GC---GGCGGAGGAAGAGGCGGAGAAGATGGTGAAGGTGGGGTTTGGGGAACACACAGAC
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Pred. No. 5e-113;
0; Mismatches 327;
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Best Local Similarity 66.0%;
Matches 669; Conservative
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LENGTH: 1403
TYPE: DNA
ORGANISM: Glycine max
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US-09-338-842A-1350
; Sequence 1350, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Wang, Xun
; APPLICANT: Wang, Xun
; APPLICANT: Wang, Xun
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; TILLE REPREBUCE: SCRIP1300-3
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR PILING DATE: 2001-01-16
; PRIOR PILING DATE: 2001-01-6
; PRIOR FILING DATE: 2001-01-6
; PRIOR PILING DATE: 2001-01-6
; PRIOR FILING DATE: 2001-01-6
; PRIOR PILING DATE: 2001-01-6
; PRIOR FILING DATE: 2001-01-6
; PRIOR FILING DATE: 2001-01-6
; PRIOR FILING DATE: 2001-01-16
                                               986 TGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAGCTGATAATAGGCTTGCCCCTTTC 1045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 GAGCAGGAGGCTATTGGCTTCTTCGCCTCAGTCTCTTAAAACCGGGCCGGTCCA 270
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868 GCACCATTGCCATGCCTTGTCCCTGAGCAAGATGATTGGCTTTACAAAGAATTCACTTGG 927
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                                                                                                 928 TCTCAATACAAATCTTCTGCTTACAAGTCTAAGCTTGGTGATTATAGACTTGGTCTCTTT
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Pred. No. 2.8e-113;
0; Mismatches 306;
                                                                                                                                                  1046 CAGAAATCTGCTGCTGATTAACCAAACACAC 1076
                                                                                                                                                                                                  988 GAGAACAACCTCTTCTCAATCATAAAACCC 1018
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US-09-938-842A-1350
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Best Local Similarity 66.8%;
Matches 622; Conservative
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                                                                                                                                                                                                               18;
                                                                                                                                                                                     Length 1403;
APPLICANT: Logusch, Sherry J.
APPLICANT: Bacrson, Scott R.
TITLE OF INVENTION: Methods for Controlling Gibberellin Levels
FILE REPERENCE: 11999.0216.DVUS01 (MOBT:216-1)
CURRENT APPLICATION NUMBER: US/10/401,321
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.2
SEQ ID NO 64
LENGTH: 1403
                                                                                                                                                                                                               Indels
                                                                                                                                                                                     32.2%; Score 424.8; DB 6; llarity 66.0%; Pred. No. 5e-113; Conservative 0; Mismatches 327;
                                                                                                                                  ; TYPE: DNA
; ORGANISM: Glycine max
US-10-401-321-64
                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                     Query Match
Best Local S
Matches 669
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                                         CATGGTGTTCCATTGGAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAA
                                                                                             AAATCTCAGTCCGAGAAAGACAGAGCTGGTCCCCCCGACCCTTTCGGCTATGGTAGCAAG
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592 661 868 892 958 AGTGATTCGTGCTTCAGGTTGAACCACTACCCGCCTTGCCCTGAGGTGCAAGCACTGAAC 652 718 712 772 838 832 caaaacargaragggririggagaacacacgacccacaaarcarrrcrcracrraggrcc 778 TITIAAAAGTGTAAAGCATAGGGTTTTTGGCTGACAACGAAGTCAAGGTTATCAATGATC TITCGAAGIGIGAAACACAGAGITITGACAAATGGATITAAGICIAGACICICAAIGAIT GCAGAAGGATTGAAGATACAACAAAAATGTGTTTAGCAAGCTTCTTATGGATAAAGAG GATCACAAATCTTTCTTCATAAATGTTGGTGATTCTCTTCAGGTTATGACCAATGGAAGG Agredaction and a series and a series of the CGGAATTTGGTTTGGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCT AACAATACTTCAGGCCTTCAGATTTTTTTTTAGAGATGGAAACTGGATTTCAGTCCCACCT GATCAGACTTCCTTTTTCATCTTGGTGACGCTCTACAGGTAATGACTAATGGGAGG AACAGCACATCTGGCTTGCAAATCTGTCTCACAGATGGCACTTGGGTTTCAGTCCCACCT 179 839 899 719 713 773 833 g 셤 ò 셤 ò a ઠે

Sequence 64, Application US/10401321
Publication No. US20030233679A1
GENERAL INFORMATION:
APPLICANT: Brown, Sherri M.
APPLICANT: Heck, Gregory R.
APPLICANT: Hilber, Kenneth J.
APPLICANT: Elich, Tedd D.
APPLICANT: Elich, Tedd D.
APPLICANT: Rao, Sudabathula
APPLICANT: Rao, Sudabathula
APPLICANT: Ream, Joel E.

US-10-401-321-64

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535 GGAGGGGTTGGGGATAAGGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAG
                                                     632 AGAAGGGTTGAAGATTCAGCAAAAGGATGTGTTTAGCAAGCTTCTAATGGATAAACAAAG
                                                                                                                595 TGATTCGTGCTTCAGGTTGAACCACTACCCGCCTTGCCCTGAGGTGCAAGCACTGAAACCG
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SEQUENCE 9, Application US/10670454

Publication No. US20040229357A1

GERREAL INFORMATION:

APPLICANT: Thomas, Stephen G

APPLICANT: Hedden, Peter

APPLICANT: Phillips, Andrew L

TITLE OF INVENTION: Gibberellin 2-Oxidase

FILE REFERENCE: 0623.0970000

CURRENT APPLICATION NUMBER: US/10/670,454

CURRENT FILING DATE: 2003-09-26

PRIOR PILING DATE: 2000-12-08

PRIOR PILING DATE: 1999-06-11

PRIOR PILING DATE: 1999-06-11

PRIOR PILING DATE: 1998-06-12

PRIOR PILING DATE: 1998-06-13

PRIOR PILING DATE: 1998-07-15

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PatentIn Ver. 2.1

SERICTH: 1008
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US-10-670-454-9
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Fublication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NOS: 285684
                                                                 959 TACTITIGGAGGICCACCATIGAGIGAAAAAAAGTACCATIATCTICACTIAIG---AAA 1015
                                                                                                                                        GGAGAGGAGTGTTTGTACAAAGAGTTCACATGGTGTGAATACAAGAAGGCTGCGTACACT 1012
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Pred. No. 4.7e-105;
0; Mismatches 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT3847_119826C.1
US-10-424-599-21951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 64.2%;
Matches 650; Conservative
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US-10-424-599-21951
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                                                                                                                                                                                                                                                                                                                                                                Length 1318;
                                                                                                                                                                                                                                                                                                                                                                  27.1%; Score 356.6; DB 8; Length 63.2%; Pred. No. 4.7e-93; ive 0; Mismatches 329; Indels
PRIOR APPLICATION NUMBER: US/09/719,108
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: PCT/GB99/01857
PRIOR PILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: GB 9812821.8
PRIOR PILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 16
SOFWARE: Patentin Ver. 2.1
SEQ ID NO 5
                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature

// ICCATION: (1243, 1265)

// OTHER INNORMATION: unidentified residue

US-10-670-454-5
                                                                                                                                                                                                    LENGTH: 1318
TYPE: DNA
ORGANISM: Arabidopsis thaliana
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Matches 586; Conservative
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                               GAGTTTGGGTTCTTCAAAGTCATCAACCATGGGGTCCGACCCGATCTTTTGACTCAGTTG
                                                                                                              GAGCAAGAAGCCATCAACTTCTTTTGCATCACTCTCTCAAAGACAAAGCGGCTCCA
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           GACTICGGCTICTICAAGCTIGIGAACCAIGGIGITCCATIGGAGTIAAIGGCCAAITIA
                                                                              GAAAACGAGGCCCTCAGGTTCTTTAAAAATCTCAGTCCGAGAAAAACAGAGCTGGTCCC
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Publication No. US20040229357A1
GENERAL INFORMATION:
APPLICANT: Homas, Stephen G
APPLICANT: Hedden, Peter
APPLICANT: Phillips, Andrew L
TITLE OF INVENTION: Gibberellin 2-Oxidase
FILE REFERENCE: 0623.0970000
CURRENT APPLICATION NUMBER: US/10/670,454
CURRENT FILING DATE: 2003-09-26
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US-10-670-454-5
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VS-10-437-963-78659

VS-10-437-963-78659

Sequence 78659, Application US/10437963

Publication No. US20040123343A1

Publication No. US20040123343A1

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 78659

LENGTH: 1260
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                              429 AATCACTTTGCATTTTCCGAGAAAATCCTCATCATTTCAGGGCGGTGGTGGAGAACTACA
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                                                                                                                                                                  416 TCTCGGGGGTGCGGAAGGTGGCGGTGCGGTGATGAAGGCGATGTCGGAGGGGTTGGAG
                                                                                                                          TTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTTGATGGCGGGGGGGTTTGGG
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US-10-437-963-78659
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ORGANISM: Oryza sativa
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APPLICANT: Matsuoka, Makoto
APPLICANT: Matsuoka, Makoto
APPLICANT: Matsuoka, Makoto
APPLICANT: Sakai, Masatomo
APPLICANT: Sakaico, Tomoaki
APPLICANT: Sakai, Miho
TITLE OF INVENTION: GIBBERELIN 2-OXIDASE GENE, FUNCTIONS AND USES THEREOF
FILE REFERENCE: SAZ-014
CURRENT APPLICATION NUMBER: US/10/392,325
CURRENT APPLICATION NUMBER: US/203-03-08
NUMBER OF SEQ ID NOS: 7
PRIOR APPLICATION NUMBER: JP 2002-276051
PRIOR FILING DATE: 2002-09-20
SOFTWARE: Patentin version 3.1
LENGTH: 984
                                                                                                                                                                          963 GTTTGTACAAAGAGTTCACATGGTGTAAATACAAGAAGGCTGCGTACACTTCAAGGCTAG 1022
                         795 TGAGGCATAGGGTTTTAGCTAACTGTAAAAAATCTAGGGTTTCTATGATTTACTTCGCTG 854
                                                                                                                          855 GACCTTCATTGACTCAGAGAATCGCTCCGTTGACATGTTTGATAGACAATGAGGACGAGA 914
                                                                                                                                                                                                                        69 TGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAAACCATTCAAGTCCA 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGACAGAGCTGGTCCCCCCGACCCTTTCGGCTATGGTAGCAAGAGGATTGGCCCAAACG 368
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                                                                                                                                                                                                                                                                        CTGATAATAGGCTTGCCCCTTTCCAGA 1049
                                                                                                                                                                                                                                                                                                                      crearaaraecrircaacaarregaaa 1001
Sequence 3, Application US/10392325 Publication No. US20040060080A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Oryza sativa
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OTHER INFORMATION:
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LOCATION: (1)
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US-10-425-115-69575

i) Sequence 69575, Application US/10425115

j) Publication No. US20040214272A1

j) Publication No. US20040214272A1

j) APPLICANT: La Rosa, Thomas J.

j) APPLICANT: Kovalic, David K.

j) APPLICANT: Thou, Yihua

j) APPLICANT: Thou, Yihua

j) TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

j) TITLE OF INVENTION: Plants

j) TITLE OF INVENTION: NUMBER: US/10/425,115

j) CURRENT APPLICATION NUMBER: US/10/425,115

j) CURRENT FILING DATE: 2003-04-28

j) NUMBER OF SEQ ID NOS: 369326

j) SEQ ID NO 69575

j) LENGTH: 1611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 ACAACAACCATGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAAACCA
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Pred. No. 4.8e-81;
0; Mismatches 397; Indels
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58.9%;
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586; Conservative
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ORGANISM: Zea mays
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Best Local S
Matches 586
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               896 TTTGGAGGACCAGCGTTGAGTGAAAATATAGCACCTTTACCTTCAGTGATGTTAAAAGGA 955
820 ACCTCCGGCCTGCAGATCGCGCTCCGCGACGGCGCGCAGTGGGTCTCCGTGCCCTCCGAC 879
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Search completed: December 28, 2005, 01:23:05 Job time : 1242.83 secs

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions .rnpbm (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions .rapbm (Published_Applications_AA_Main) and .rapbn (Published_Applications_AA_New).

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Result
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Maximum Match 100%
Listing first 45 summaries
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                                             56.4
40.8
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seq length: 2000000000
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1: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*

8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*

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                  GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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7 US-11-152-892-5

6 US-10-750-185-48573

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7 US-11-152-892-2

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7 US-11-112-908-45

6 US-10-995-561-1331

6 US-10-997-4377A-1

6 US-10-995-561-52521

6 US-10-995-561-52521

6 US-10-750-185-53362

7 US-11-121-086-46

7 US-11-121-086-48

8 US-10-950-185-33828

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10 US-11-121-086-52

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Sequence 59293, A
Sequence 796, App
Sequence 31828, A
Sequence 13293, A
Sequence 61, Appl
Sequence 52, Appl
Sequence 42851, A
Sequence 1, Appli
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Sequence 1, Appli
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Sequence 48573, A
Sequence 71, Appli
Sequence 3, Appli
Sequence 13286, A
Sequence 13286, A
Sequence 44, Appl
Sequence 45, Appl
Sequence 13112, A
Sequence 1, Appli
Sequence 64795, A
Sequence 52521, A
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Sequence 4305, Ap	Sequence 103, App	Sequence 15, Appl	Sequence 28226, A	Sequence 73, Appl	Sequence 55, Appl	Sequence 72, Appl	Sequence 211, App	Sequence 34028, A	Sequence 19, Appl	Sequence 54120, A	Sequence 13503, A	Sequence 42377, A	Sequence 47560, A	Sequence 48102, A	Sequence 2, Appli	Sequence 127, App	Sequence 57430, A	Sequence 212, App	Sequence 13278, A	Sequence 37195, A	Sequence 64, Appl

ALIGNMENTS

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Sequence 5, Application US/11152892

Publication No. US20050251883A1

GENERAL INFORMATION:

APPLICANT: Amasino, Richard M.

APPLICANT: Schomburg, Fritz M.

APPLICANT: Schomburg, Fritz M.

APPLICANT: Michaels, Scott D.

APPLICANT: Bizzell, Colleen M.

TITLE OF INVENTION: Dwarfism Genes and Dwarf Plants

FILE REFERENCE: 960296.97605

CURRENT APPLICATION NUMBER: US/11/152,892

CURRENT APPLICATION STEEL COLLEGE COL
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PRIOR FILING DATE: 2002-05-23
NUMBER OF SEQ ID NOS: 12
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 1017
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Best Local Similarity 55.7%;
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                                                                                        ATATAGCACCTTTA 934
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TTATAGAGTGTTCA
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                                                                                                 Query Match
Best Local S
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Publication No. US20050266459A1

GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: 09188.6000-0000

FILE REFERENCE: 09138.6000-0000

CURRENT APPLICATION NUMBER: US/11/121,086

CURRENT FILING DATE: 2005-05-04

CURRENT FILING DATE: 2005-05-04
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CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 48573
LENGTH: 3159
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LENGTH: 164527
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APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
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APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/567,570 PRIOR FILING DATE: 2004-05-04
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149090 TGCTTÄATAAAATGTÄACAGTAACTTTTGCTATCTTTAAGAAGTGGGATTATAGGTGATT 149149
                                     1060 TGATTAACCAAACACCCTTCAAATTCCACTCATTTTACGCACGTGTTATTACCCCAAT 1119
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Similarity 52.0%;
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KERR, Richard
ROSENFELD, David
HOLM, Tom
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52.3%; Pred. No. 0.
                                                                              Score 40.6; DB Pred. No. 2.4; 0; Mismatches
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                                                                                                                       DB 7;
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APPLICANT: Amasino, Richard M.
APPLICANT: Schomburg, Fritz M.
APPLICANT: Michaels, Scott D.
APPLICANT: Mizzell, Colleen M.
ITILE OF INVENTION: Dwarfism Genes and Dwarf Plants
FILE REFERENCE: 960296.97605
CURRENT APPLICATION NUMBER: US/11/152,892
CURRENT FILING DATE: 2005-06-15
PRIOR APPLICATION NUMBER: US/10/155,435
PRIOR APPLICATION NUMBER: US/10/155,435
NUMBER OF SEQ ID NOS: 12
SOFTWARB: Patentin Ver. 2.1
SEQ ID NO 2
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Matches
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Best Local S
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APPLICANT: Michaels, Scott D.
APPLICANT: Michaels, Scott D.
APPLICANT: Bizzell, Colleen M.
TITLE OF INVENTION: Dwarfism Genes and Dwarf Plants
FILE REFERENCE: 960296.97605
CURRENT PEDLICATION UNMEER: US/11/152,892
CURRENT FILING DATE: 2005-06-15
PRIOR APPLICATION UNMEER: US/10/155,435
PRIOR FILING DATE: 2005-03
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Amasino, Richard M.
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                      TYPE: DNA
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ORGANISM: Arabidopsis
                                          LENGTH: 3861
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Pred. No. 0.17;
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ORGANISM: Homo sapiens
FEATURE:
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1):..(1125000)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-US-10-995-561-13286
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US-10-995-561-13286
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                                                                                                                                           US-11-112-908-44/c
Sequence 44, Application US/11112908
Publication No. US20050260659A1
GENERAL INFORMATION:
APPLICANT: Harris, Cole
APPLICANT: Davis, Lisa M.
TITLE OF INVENTION: Breast Cancer B
FILE REFERENCE: 04-164-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 13286
LENGTH: 1125000
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Publication No. US20050272054A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
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Best Local Similarity
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Best Docal Similarity 50.5%;
Matches 95; Conservative
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CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
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Pred. No. 19;
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                         Biomarkers
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CURRENT APPLICATION NUMBER: US/11/112,908
CURRENT FILING DATE: 205-04-22
PRIOR APPLICATION NUMBER: US 60/564,758
PRIOR FILING DATE: 2004-04-23
PRIOR PELICATION NUMBER: US 60/575,978
PRIOR PRIOR PELICATION NUMBER: US 60/631,702
PRIOR PELICATION NUMBER: US 60/631,702
PRIOR PELICATION NUMBER: US 60/631,702
PRIOR PELICATION NUMBER: US 60/631,826
PRIOR PELICATION NUMBER: US 60/633,826
PRIOR PELICATION NUMBER: 
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PRIOR FILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: US 60/631,702
PRIOR FILING DATE: 2004-11-30
PRIOR APPLICATION NUMBER: US 60/633,826
PRIOR FILING DATE: 2004-12-07
NUMBER OF SEQ ID NOS: 511
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 44
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US-11-112-908-45/c
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Publication No. US20050260659A1
GENERAL INFORMATION:
APPLICANT: Harris, Cole
APPLICANT: Davis, Lisa M.
TITLE OF INVENTION: Breast Cancer Biomarkers
FILE REFERENCE: 04-164-US
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Best Local (
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CURRENT FILING DATE: 2005-04-22
PRIOR APPLICATION NUMBER: US 60/564,758
PRIOR FILING DATE: 2004-04-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 182314
TYPE: DNA
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                       65032 ACAAAATAAAGCAAAGAGTGTTAGTTGATACAAAATAATCAACATTTTACAGTATGGAT
64972 GATTTAGGAGTAATGATGATGATGATATACAATTTTTATTTTATTTTATTTTA 64919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2392 ACAAAATAAAGCAAAGAGTGTTAGTTGATACAAAATAATCAACATTTTACAGTATGGAT 2333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2332 GATTTAGGAGTAATGATGACTGATGATATACAATTTTTATTTTATTTTATTTTA 2279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 896 TTTGGAGGACCAGCGTTGAGTGAAAATATAGCACCTTTACCTTCAGTGATGTTA 949
                                                                                                                                                                                                           836 AAAAGTGTAAAGCATAGGGTTTTGGCTGACACAACGAAGTCAAGGTTATCAATGATCTAC
                                                                                                                                                                                                                                                                                      67; Conserv
                                                    TTTGGAGGACCAGCGTTGAGTGAAAATATAGCACCTTTACCTTCAGTGATGTTA 949
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                                                                                                                                                                                                                                                                                                                    2.9%;
                                                                                                                                                                                                                                                                                  Score 38.8; DB Pred. No. 8.5; 0; Mismatches
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Pred. No. 7.6;
0; Mismatches
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RESULT 9

US-10-995-561-13312

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US-10-995-561-13312
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13312
LENGTH: 130472
TYPE: DNA
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publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RES
TITLE OF INVENTION: DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                      SEQ ID NO 1
LENGTH: 1258
TYPE: DNA
ORGANISM: homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10997437A Publication No. US20050250184A1
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FILE REFERENCE: 03-16
CURRENT APPLICATION NUMBER: US/10/997,437A
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: 60/525,597
PRIOR FILING DATE: 2003-11-26
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                      -10-997-437A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
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Local Similarity 50.6%;
nes 119; Conservative
                                                                                                                                                                                                                             match 2.9%;
Local Similarity 51.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59834 ATACCTTTAAACCAGTCCCATATTGTGCCCCTCCTCAACCTGATTCCCCCTTCTTCATTGC
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                                                                                  1203 AGATGTTTATCATTTTCTTTTTCTTGTTTCATCTAAGTGTAACAGTTGGTCTCAACTTCC 1262
                                                                                                                          1072 TATTTGGAACGGCATGAAAATTAAAATTTCGGTCATGTTTTAGAGACAGTGGAGTGTAA
                                                                                                                                                                     1143 TGTCTGTCTAGGTTTCAAACAGTTGACTCTACTTGACATATATAGAAAATGAATAGGTTA 1202
                                                                                                                                                                                                                 90;
ATCTGTGGCTAATTCTGTTGGTCGTTTGTATTATAAATGTAAAATAGTATTCCAGCTATT 1191
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Pred. No. 8;
0; Mismatches 114; Indels
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Sequence 52521, Application US/10995561

Publication No. US20050272054A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT APPLICATION DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastESQ for Windows Version 4.0
TYPE: DNA
COLUMN USES CLOSES
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US-10-995-561-52521
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; ORGANISM: Bovine
US-10-750-185-64795
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                                                                                                                                    ; ORGANISM: Homo sapiens 
US-10-995-561-52521
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                                                                            Query Match 2.8%;
Best Local Similarity 53.4%;
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Best Local Similarity
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SEQ ID NO 64795
LENGTH: 4873
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APPLICANT: MMI GENOMICS, INC.
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                                                             Matches
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CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
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TITLE OF INVENTION: COMPOSITIONS FOR INFERRING
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1118 ATTITCTTTCCTTTTTCCTGTGTCTGTCTAGGTTTCAAACAGTTGACTCTACTTG 1177
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                                                             Conservative
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Pred. No. 2.5;
                                                           Score 37.2; DB Pred. No. 0.42; 0; Mismatches
                                                                                            DB 6;
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US-11-121-086-46

Sequence 46, Application US/11121086

Sequence 46, Application US/11121086

Publication No. US20050266459A1

GENERAL INFORMATION:
APPLICANT: PIELSEN, KIRGTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000

CURRENT APPLICATION NUMBER: US/11/121,086

CURRENT FILING DATE: 2005-05-04

PRIOR APPLICATION NUMBER: 60/567,570

PRIOR APPLICATION NUMBER: 60/567,570

PRIOR TILING DATE: 2004-05-04

PRIOR TILING DATE: 2004-05-04

PRIOR SEQ ID NOS: 107

SOFTWARE: Patentin version 3.3
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Sequence 53362, Application US/10750185
Publication No. 100050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIN version 3.1
SEQ ID NO 53362
LENGTH: 2555
TYPE: DNA
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                                                          SEQ ID NO 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
ORGANISM: Homo sapiens
                                       ENGTH: 158410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1165 TTGACTCTACTTGACATATATAGAAAATGAATAGGTTAAGATGTTTATCATTTTCTTTTT 1224
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KERR, Richard
ROSENFELD, David
HOLM, Tom
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PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 59293
LENGTH: 1276
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Publication No. US20050260603A1
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Best Local
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CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
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APPLICANT:
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les 71; Conserv
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                              1249 TGGTCTCA 1256
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TTATCTCA 367
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KERR, Richard
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Search completed: December 28, 2005, 01:30:10 Job time : 242.513 secs

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AB181373 Vigna ang
AB031206 Lactuca B
AR452812 Sequence
AR528430 Sequence
AR528430 Sequence
AB125233 Nicotiana
AF100955 Pisum sat
AF101382 Pisum sat
BD243014 Bnzyme. 7
AR44996 Sequence
AJ132437 Arabidops
AB067639 Daucus ca
AR452818 Sequence
BT00225 Triticum
BT002153 Arabidops
AR44994 Sequence
BD243012 Enzyme. 7
AR44994 Sequence
AX008675 Sequence
AX008675 Sequence
AX008675 Sequence
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Spermatophyta, Magnollophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
Phaseolus.
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AR44995 Sequence
AX008677 Sequence
BT002987 Arabidops
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Dna constructs and methods to enhance the production commercially viable transgenic plants

Patent: WO 2004092390-A 3 28-OCT-2004;

Monsanto Technology LLC (US)

Location/Qualifiers
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100.0%; Pred. No. 2.1e-291;
ive 0; Mismatches 0; Indels
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/organism="Phaseolus coccineus"
/mol_type="unassigned DNA"
/db_xref="taxon:3886"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
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                                                                                                                                                                                                                       AR452818
BT009225
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AY085539
ATH132435
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AR526430
AR125233
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Matches
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AB181372 Vigna ang
AR528429 Sequence
AY588978 Nerium ol
AY588978 Nerium ol
AY594292 Nerium ol
AJ315663 Cucurbita
AJ302041 Cucurbita
AB125232 Nicotiana
Y09113 M.macrocarp
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BTO04464 Arabidops
A1132436 Arabidops
BD243013 Enzyme. 7
                                                                                           December 27, 2005, 17:31:33 ; Search time 5300.67 Seconds (without alignments) 10680.938 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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               version 5.1.6
- 2005 Compugen Ltd.
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AR44901
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PCO132438
AB181372
AX588978
AY584292
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AX506655
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AX651428
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Maximum Match 100%
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L Patent: JP 2002518005-A 1 25-JUN-2002;
THE UNIVERSITY OF BRISTOL
OS Phaecolus occidines (scarlet runner bean)
PN JP 2002518005-A/1
PD 25-JUN-2002
PF 11-JUN-1998 GB 981281.8 J5-JUL-1998 GB 9815404.0 PI
STEPHEN GREGORY THOWAS, PETER HEDDEN, ANDREW LEONARD PHILLIPS PC
C12N15/04, A01H5/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N5/10, PC
C12N15/09,
PC C12NN5/00, C12NN5/00, C12N15/00
CC Enzyme Location/Qualifiers
FT source Location/Qualifiers
FT source /organism='Phaseolus coccineus (scarlet runner

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/organism='Phaseolus coccineus (scarlet runner

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Bukaryota, Viriliplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viriliplantae; Streptophyta; Embryophyta; Core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.

1 (Dases I to 1318)
Thomas, S. G., Hedden, P. and Phillips, A.L.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosida, eurosida I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
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120 ACGCCTTGTTCACGGGGATTCCTGTGGTCGACCTCACGCACCACGATGCCAAGAATCTC 187
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                                                                       TTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTGTAAAG
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Best Local Similarity 100.0%; Pred. No. 2.2e-291;
Matches 996; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Unclassified.
Unclassified.
Unclassified.
Thomas, S.G., Hedden, P. and Phillips, A.L.
Gibberellin 2-oxidase
Patent: US 6670527-A 1 30-DEC-2003;
The University of Bristol; Bristol;
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Sequence 1 from patent US 6670527.
AR444991
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/translation="MVVLSQPALNQFFLLKPFKSTPLFTGIPVVDLTHPDAKNLIVNA
CRDFGFFKLVNHGVPLELMANLENEALRFFKKSQSEKDRAGPPDPFGGSKRIGPNGD
VGWVEYLLLANTNPDVISPKSLCIFRENPHHFRAVVENYITAKNMCYAVLELMAEGLG
IRQRYLLSRLLKDEKSCFRLMHYPPCPEVQALMRNLVGFGEHTDPQIISVLSNST
SGLQICLTDGTWVSVPPDQTSFFINVGDALQVMTNGRFKSVKHRVLADTTKSRLSNIT
FGGFPALSENIAPLPSVMLKGEECLIXEFTWGEYKKAAYTSRLADNRLAPPQKSAAD"
                                          PLN 20-APR-1999
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                                                                        AJ13438
AJ13438
AJ 20438.1 GI:4678885
AJ 204304399: gaox1 gene.
Phaseolus coccineus
Phaseolus coccineus
Bukaryota; Virialplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Pabales; Pabaceae; Papilionoideae; Phaseoleae;
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Molecular cloning and functional expression of gibberellin oxidases, multifunctional enzymes involved in gibberellin deactivation
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                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 1318)
Phillips, A.L.
Direct Submission
Submitted (18-JAN-1999) Phillips A.L., Plant Sciences,
Ashton Research Station, Long Ashton Research Station,
BS41 9AF, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1318;
                                        mRNA linear PLN
2-oxidase, gene ga2ox1.
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/dev stage="Late developing seeds"
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llarity 100.0%; Pred. No. 2.2e-291;
Conservative 0; Mismatches 0;
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/db_xref="G1:4678586"
/db_xref="G03:Q9XG83"
/db_xref="UniProt/TrEMBL:Q9XG83"
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    /organism="Phaseolus cc/mol_type="mRNA"
    /db_xref="taxon:3886"

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  6; Length 1318;
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Query Match
100.0%; Score 996; DB 6; I
Best Local Similarity 100.0%; Pred. No. 2.2e-291;
Matches 996; Conservative 0; Mismatches 0;
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/trānslation="MVVLSQPALNQPLLLKPCKSTPLFTGIPVVDFTHPDAKNLIVEA
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IAQNYLSRLLKDEKSGEKSTRMNHYPPCPEVPALNRLVGFGHTDPQIISVLRSNST
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FGGPALSEKIAPLPSVWVKGEESLYKEFTWWEYKKAAYTSRLADNRLAPFEKSATD"
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Tokyo, Dept. Appl. Biol. Chem., Fac. of Agriculture; 1-1-1 Yayoi, Bunkyo, Tokyo, 113-8657, Japan (E-mail:nkjm@pgrl.ch.a.u-tokyo.ac.jp, Tel:81-3-5841-5192, Fax:81-3-5841-8025)
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.larity 95.3%; Pred. No. 1.8e-268;
Conservative 0; Mismatches 47; Indels 0;
                                                                                  1. .1360

/organism="Vigna angularis"

/organism="Vigna angularis"

/ol type="mRNA"

/cultivaz="bainagon"

/db xref="taxon:3914"

/dow stage="etiolated epicotyl"

/country="Japan"
                                                                                                                                                                                                                                                                                                         /evidence=experimental
/product=gibberellin 2-oxidase"
/protein id="BAD9567.1"
/db_xref="G1:67077812"
                                                                    Location/Qualifiers
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/gene="VaGA20xA1"
83. .1081
/gene="VaGA20xA1"
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Unpublished
2 (bases 1 to 1360)
Nakajima,M., Xu,Z., Park,S., Tomioka,K., Sakane,M. and Yamaguchi,I. Buret Submission
Direct Submission
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Vigna angularis VaGA20xA1 mRNA for gibberellin 2-oxidase, complete
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                                    ATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTGATGGCGGAGGGGTTGGGG
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     AAAGACAGAGCTGGTCCCCCCGACCCTTTCGGCTATGGTAGCAAGAGGATTGGCCCAAAC
                                                                                                                                                                       ATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTGATGGCGGAGGGGTTGGG
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2 (bases 1 to 1245)
2 (bases 1 to 1245)
2 (bases 1. Garcia-Martinez,J.L. and Lopez-Diaz,I.
Direct Submission
Submitted (08-APR-2004) Instituto de Biologia Molecular y Celular
de Plantas, Consejo Superior de Investigaciones Cientificas (CSIC),
Universidad Politecnica de Valencia, Avda. de los Naranjos s/n,
Valencia 46022, Spain
Location/Qualifiers
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1 (bases 1 to 1245)
Ubeda-Tomas,S., Garcia-Martinez,J.L. and Lopez-Diaz,I.
Isolation, characterization and multi-site polyadenylation
20-oxidases and GA 2-oxidases in Nerium oleander
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al Similarity 68.0%; Pred. No. 2.5e-129;
677; Conservative 0; Mismatches 312; Indels
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/organism="Nerium oleander"
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/product="GA_2-oxidase_2"
/protein_id="AAT92094.1"
/db_xref="GI:51011366"
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Submitted (02-APR-2004) Instituto de Biologia Molecular de Plantas, CSIC/Universidad Politecnica de Valencia, Avda de los Naranjos sn, Valencia 46022, Spain
Location/Qualifiers
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0; Mismatches 266; Indels 6;
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/protein_id="AAT72916.1"
/db_xref="G1:50293061"
                                                                                                                                                                                                                                                                                                                                                      /gene="GA2ox3"
/note="GA 2-oxidase; NoGA2ox3"
                                                                                                                                              /organism="Nerium oleander"
/mol_type="mXNA"
/db_xref="taxon:63479"
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1383 bp mRNA linear PLN 19-JUN-2003 maxima partial mRNA for Gibberellin 2-oxidase (ga2ox

ÄJ315663 AJ315663.1 GI:32127336

ACCESSION VERSION

CMA315663 Cucurbita

DEFINITION RESULT 10 CMA315663 LOCUS

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/ LTAIN 1 AT 101 = "MAAASSPSAAFYSGI PLIDLSAPDAKQLIVKACEELGFFKVVKH
GVPMELISSLESESTKFFSLPLSEKQRAGPPSPFGVGNKQIGRNGDVGWVEYLLLNTH
LESNBOGFLSI FGQDPQKLRSAVNDY ISAVRNAAGEI LELMAEGLKI QQRNVFSKLVM
DEQSDSVFRVHYYPRPCPDLQALKGTNMIGFGFHTPPQI ISVLRSNNTSGFQI SLADGN
WISVPPDHSSFPINVGDSLQYMTNGRFKSVKHRVLTNSSKSRVSMI YFGGPPLSEKIA
PLASLMQGEERSLYKEFTWFEYKRSAYNSRLADNRLVPFERIAAS"
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                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
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                                                                                                                                                                                           Frisse, A. and Lange, T. Gibberellin biosynthesis in young seedlings of Cucurbita maxima Unpublished
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GERMANY
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/function="2-oxoglutarate dependent dioxygenase"
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46.3%; Score 461.2; DB 15; Length 1383;
Best Local Similarity 69.0%; Pred. No. 1.6e-128;
Matches 647; Conservative 0; Mismatches 288; Indels 3;
                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (19-707-2001) Lange T., Botanical Institute,
Braunschweig, Mendelssohnstr. 4, D-38106 Braunschweig,
related entry AJ315662.
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/product="Gibberellin 2-oxidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Cucurbita maxima"
/mol type="maXNA"
/culfivar="Riesenmelone, gelb ge
/db xref="taxon:3661"
/clone="2beta-WS2"
/tissue_type="root tips"
/dow stage="7 day old seedling"
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/db_xref="GI:32127337"
ga20x gene; gibberellin 2-oxidas
Cucurbita maxima (winter equash)
Cucurbita maxima
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function="2-oxoglutarate dependent gibberellin
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Best Local Si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (14-DBC-2000) Lange T., Botanical Institute, Dept. Plant
Physiology and Biochemistry, TU Braunschweig, Mendelssohnstr. 4,
Braunschweig, D-38106, GBRMANY
Location/Qualifiers
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developing seeds of Cucurbita maxima L
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Stress-regulated genes of plants, transgenic plants containing
same, and methods of use
Patent: WO 0216655-A 1350 28-FEB-2002;
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                                                                                                                   CACATCTGGCTTGCAAATCTGTCTCACAGATGGCACTTGGGTTTCAGTCCCACCTGATCA
                                                                                                                                             711 GACTICCITITICALCAAIGTIGGIGACGCICTACAGGIAATGACTAAIGGGAGGITTAA
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    .1026
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/db_xref="G1:1666096"
/db_xref="G0A:004162"
/db_xref="UniProt/TrEMBL:004162"
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KVINHGVPMEFISTLESESTKFFSLPLSEKQRAGPPSPFGYGNKQIGRNGDVGWVEYL
Gaskin, P., Lange, T. and Hedden, P.
Gibberellin biosynthesis from gibberellin Al2-aldehyde in endosperm
and embryos of Marah macrocarpus
plant Physiol. 113 (4), 1369-1377 (1997)
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MGEESDSVERVNHY PRCPEELQALEGTIMI GFOSHTDPQI I SVLRSNNTSGLQI SLPD
MANI SVPPDQTSPFINVGDSL,OWNTNORFKSVKHRVLINSLKSR I SANI Y FGGPPLISEK
I APLISSLMKGEBSLYKKETWFEYKRSAVNSKLADNRLVHFERI AAS."
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                                                                                                                                                                       Direct Submission
Submitted (31-OCT-1996) P. Hedden, University of Bristol,
Department of Agricultural Sciences, IACR-Long Ashton Research
Station, Long Ashton, Bristol, BS18 9AF, UK
Location/Qualifiers
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Pred. No. 7.6e-121;
0; Mismatches 265; Indels
                                                                                                                                                                                                                                                                                                                          organism="Marah macrocarpus"
                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="immature seed"
/dev_stage="immature seed"
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/db_xref="taxon:48242"
/clone="M7-3"
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Matches 656; Conservative
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                                                        Length
                                                                                Indels
                                                       Score 424.4; DB 6;
Pred. No. 2.5e-117;
0; Mismatches 291;
     /mol_type="unassigned DNA"
/db_xref="taxon:3702"
                                                       42.6%;
llarity 67.5%;
Conservative
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1. olocation/Qualifiers
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                                         GAATACCTCCTCCTCAACACCCTGATGTTATCTCACCCAAATCACTTTGCATTTTC
                                                                                                                                            ATGTGCTATGCGCTGTTGGAATTGATGGCGGAGGGCTTGGGGATAAGGCAGAGGAATACG
                                                                                                                                                           GTGTCGTACAAGGTGTTGGAGATGGTTGCCGAAGAACTAGGGATAGAGCCAAGGGACACT
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                                                                                                                                                                                               TTAAGCAGGTTGCTGAAGGATGAGAAAAGTGATTCGTGCTTCAGGTTGAACCACTACCCG
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SUMMARIES

Description	Adt62692 DNA encod	Aaz55912 Runner be	Aaz99471 Soybean g	Aad40261 Soybean G	Abz13545 Arabidops	Ada67975 Arabidops	Aaz55916 Arabidops	Adm94213 Soybean D	Adm94205 Soybean D	Aaz99472 Soybean g	Aad40262 Soybean G	Aaz55917 Arabidops	Adm94207 Wheat Dio	Aac39277 Arabidops	Aaz55915 Arabidops	Aeb67733 Rice geno	Ada70120 Rice gene	Adk00081 Rice CDNA	Aeb67784 Rice geno
ΩΙ	ADT62692	AAZ55912	AAZ99471	AAD40261	ABZ13545	ADA67975	AAZ55916	ADM94213	ADM94205	AAZ99472	AAD40262	AAZ55917	ADM94207	AAC3 9277	AAZ55915	AEB67733	ADA70120	ADK00081	AEB67784
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% Query Match	100.0	100.0	83.1	83.1	42.6	42.6	42.6	42.3	42.1	42.0	42.0	38.3	36.4	35.8	35.8	35.7	35.5	35.5	35.5
Score	966	966	827.4	827.4	424.4	424.4	424.4	421.4	419.8	418.2	418.2	381.6	362.6	356.6	356.6	355.6	354	354	354
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12 ADM94203 Rice Diox Adm94201 Corn Diox Adx29474 Adx10264 Corton gi Adx29474 Corton gi Adx29474 Corton gi Adx29474 Corton gi Adx11608 Plant ful Adx11286 Plant ful Adx29418 Corton gi Adx11286 Plant ful Adx29418 Adx29418 Plant ful Adx29417 Pl	ALIGNMENTS	ntry) B coccineus gibberellin 2-oxidase. DNA; T-DNA; Agrobacterium Ti plasmid; transgene; transgenic plant; transgenic; plant; ; ds.	.000. 159P. XGY LLC. Zhang W, Ye X;	comprising a T-DNA comprising an Agrobacterium Ti plasmid fon linked to a transgene linked to an Agrobacterium Ti octder region, useful for enhancing production of 8. D NO 3; 77pp; English. Intion relates to a DNA plasmid comprising a transfer DNA and an Agrobacterium Ti plasmid first border region linked transgene linked to an Agrobacterium Ti plasmid second and located in the DNA plasmid outside of the T-DNA is a cassette comprising a plant cell non-lethal negative
1655 1555 783 783 783 831 1322 1065 919 811 9576 403 403 406 683 683 683 683 683 683 683 683 683 68	DNA;	ent lus er D ; tx 8e;	2004WO-US011000 2003US-0461459P NTO TECHNOLOGY Krieger E, Z 349/74.	pri lii on on loc see
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selectable marker gene linked to a vector backbone DNA. Also disclosed are a method for enhancing the selection of transgenic plants that do not contain vector backbone DNA, a method for reducing the copy number of a transgene in a plant cell, and a transgenic plant produced by the method. The DNA plasmid comprises the expression cassette comprising a promoter that functions in plant cells operably linked to a plant cell non-lethal negative selection marker gene. The promoter is a constitutive promoter. The promoter expresses the linked non-lethal negative selection marker gene or regeneration. The plant cell non-lethal negative selectable marker gene comprises a plant hormone biosynthetic pathway gene, degradative gene, biosynthetic pathway gene or signalling gene, or metabolic interference biosynthetic pathway gene or signalling gene, or metabolic interference comprises a transgene of agronomic interest. The plant hormone from antiblotic resistance and herbicide resistance. The transgene comprises a transgene of agronomic interest. The plant hormone biosynthetic pathway genes, auxin pathway gene, ethylene pathway genes, and abscisic acid pathway genes. The plasmid is useful for enhancing the production of commercially viable transgenic plants. The present sequence represents bNA encoding phaseolus coccineus gibberellin produce.
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Sequence 999 BP; 263 A; 221 C; 249 G; 266 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents CDNA encoding a runner bean gibberellin (GA) 2-oxidase, PcGA2Ox1. This enzyme is a GA 2-beta-hydroxylase that acts on C19-GAs and for which 2-beta-hydroxylation is its only activity. Hydroxylation at the 2-beta position of a GA results in a biologically inactive product, and is the most important route for GA metabolism in
                                                              TTCATCAATGTTGGTGACGCTCTACAGGAAATGACTAATGGGGAGGTTTAAAAGTGTAAAAG
                      661 rrgcaaarcrececacaearcscarrecerrreagreceacercaacaerrecerrr
                                                 TTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTGTAAAG
                                                                                                                GCGTTGAGTGAAAATATAGCACCTTTACCTTCAGTGATGTTAAAAGGAGAGGAGTGTTTG
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/product= "Gibberellin 2-oxidase PcGA2ox1"
/transl_except= (pos:1058. .1063, aa:Ala)
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P-PSDB; AAY58597.
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tissues. The mucleic acids can be used to transform plants so that tissues. The mucleic acids can be used to transform plants so that tissues. The mucleic acids can be used to transform plants so that concentration of bloactive GAs in the plants and therefore to inhibit plant growth. Growth inhibition is useful in many agricultural and horticultural applications such as enhancing lodging-ceststance and grain yield in cereals, improving seedling quality, reducing the growth of amenity grasses, reducing shoot growth in orchard and ornamental trees, improving tolerance to cold, drought and infection, can dincreasing yields (by the diversion of assimilates from vegetative to corproductive organs). The nucleic acids may also be used to induce male and increasing yields (by the diversion in floral organs), prevent preceptoductive organs). The nucleic acids may also be used to induce male corproducting, reduce shoot growth in hedging plants, inhibit reversibility in the development or germination of seeds and reduce shoot growth in commercial wood species. Antisense constructs of the nucleic growth in seedless grapes, citrus fruits and pears), improve skin texture and fruit shape in apples, increase stem length and therefore yield in sugar cane, increase yield and earliness in celery and rhubarb, improve malting yields and quality in cereals (particularly barley), and increase growth in woody species
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    ensuring that the active hormones do not accumulate in plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1318 BP; 358 A; 296 C; 282 G; 382 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 996; DB 3; Length 1
Best Local Similarity 100.0%; Pred. No. 6.7e-310;
Matches 996; Conservative 0; Mismatches 0; Indels
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               TTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTGTAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Obtaining transgenic plant useful for controlling seed germination ar seedling growth comprises transgene comprising a sequence expressing altered levels of an essential hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gibberellic acid; copalyl diphosphate synthase; 3beta-hydroxylase; 2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase; seed germination; seedling growth; gibberellin biosynthetic pathway; transgenic plant; hypocotyl; epicotyl; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes a gibberellic acid 2-oxidase 1 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heck GR, Kishore GM, Logusch EW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Soybean gibberellic acid 2-oxidase 1 cDNA sequence.
                                                                                                                                                                                                                                                                                         1028 AATAGGCTTGCCCTTTCCAGAAATCTGCTGCTGAT 1063
                                                                                                                                                                                                                                                                          AATAGGCTTGCCCCTTTCCAGAATCTGCTGCTGAT 996
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Piller KJ, Rao S, Ream JE;
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P-PSDB; AAY84099.
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07-JUN-1999;
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The specification
           describes methods for the inhibition and control of gibberellic acid levels. Gibberellic acid levels may be inhibited or controlled by use of a chimeric expression construct expressing a RNA or protein which suppresses the gibberellin biosynthetic pathway sequence, diverts substrate from the pathway, or degrades pathway substrates or products. The methods uses copalyl diphosphate synthase, 3beta-hydroxylase, oxidase, phytoene synthase, C2 oxidase, and a 2beta, 3beta-hydroxylase polynucleotides to achieve this. The method is used to control seed germination and seedling growth especially to regulate gene products of gibberellin biosynthetic pathway and restoration of normal seed germination, in transgenic plants. The plants produced are gibberellin deficient, and have shortened hypocotyl and/or epicotyl phenotypes
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                                                                                                                                                                                                                                                                       Length 1359;
                                                                                                                                                                                                                                         Sequence 1359 BP; 340 A; 305 C; 304 G; 409 T; 0 U; 1 Other;
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sequence, which is used in the method of the invention.
                                                                                                                                                                                                                                                                       Score 827.4; DB 3;
Pred. No. 1.7e-255;
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89.9%;
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778 AAGCATAGGGTTTTGGCTGACACCAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGA
                                     838 CCAGCGTTGAGTGAAAATATAGCACCTTTACCTTTCAGTGATGTTAAAAGGAGAGAGTGT
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/product= "GA 2-oxidase 1 protein"
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Piller KJ, Rao S,
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                                                                                                                                                                                                                Gaps
etc., and is also useful in storage and transport of seeds to red
premature germination which may affect agronomic or food quality
seeds. The present sequence is soybean GA 2-oxidase 1 cDNA
                                                                                                                                                                                                          3,
                                                                                                                                                    Query Match
83.1%; Score 827.4; DB 6; Length 1359;
Best Local Similarity 89.9%; Pred. No. 1.7e-255;
Matches 898; Conservative 1; Mismatches 97; Indels 3;
                                                                                                         Sequence 1359 BP; 340 A; 305 C; 304 G; 409 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                              1 ATGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTT
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                                                                                                                                                          Query Match
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The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell producting a profile of expressed polynucleotides in the plant cell production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsia thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
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Pred. No. 1.5e-125;
0; Mismatches 291; Indels 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 144; SEQ ID NO 1350; 577pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana stress regulated gene SEQ ID NO 1350
958 GATAATAGGCTTGCCCCTTTCCAGAAATCTGCTGCTGAT 996
1062 GATAATAGACTCGGCCCTTTTGAGAAATCTGCTGCTGAT 1100
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26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
                                                                                                                                                                                                                                                             ABZ13545 standard; DNA; 1026
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al Similarity 67.5%;
612; Conservative
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Goff Z.

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Glazebrook Whitham S,

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Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                 present invention relates to a method (MI) for identifying genes
                                                                                                                               6; SEQ ID NO 223; 899pp; English.
                  (SYGN ) SYNGENTA PARTICIPATIONS AG
22-JUN-2001; 2001WO-IB001105
                                                                WPI; 2003-175290/17
                                                                                                             expression.
                                   Chang H,
Katagiri
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                                                                         CGAGAAAATCCTCATCATTCAGGGGGGGGTGGTGGAAACTACATTACAGCAGTGAAGAAC
                                                                                                             ATGTGCTATGCGGTGTTGGAATTGATGCCGGAGGGGTTGGGGATAAGGCAGAGGAATACG
                                                                                                                                                  TTAAGCAGGTTGCTGAAGGATGAGAAAAGTGATTCGTGCTTCAGGTTGAACCACTACCCG
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involved in plant resistance or response to pathogenic infection. Mi comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an unlinfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction, (ml) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
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Pred. No. 1.5e-125;
0; Mismatches 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 42.6%;
Best Local Similarity 67.5%;
Matches 612; Conservative
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Plant; bacterial infection; fungal infection; viral infection; SEQ ID 223

Arabidopsis thaliana gene,

Arabidopsis thaliana

WO2003000898-A1

03-JAN-2003

(first entry)

20-NOV-2003

22-JUN-2001; 2001WO-IB001105

BP.

1026

DNA;

ADA67975 standard;

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cornulate in plant tissues. The nucleic acids can be used to transform plants so that gibberellin 2-oxidase can be constitutively over-expressed cor otherwise enhanced to reduce the concentration of bloactive GAs in the plants and therefore to inhibit plant growth. Growth inhibition is useful in many agricultural and horticultural applications such as enhancing coloding-resistence and grain yield in cereals, improving seedling capality, reducing the growth of amenity grasses, reducing shoot growth in orchard and ornamental trees, improving tolerance to cold, drought and cornand increasing yields (by the diversion of assimilates from vegetative to reproductive organs). The nucleic acids may also be used to induce male and/or female sterility (by expression in floral organs).

Contact prevent preverse sprouting, reduce shoot growth in hedging plants, inhibit reversibility in the development or germination of seeds and reduce shoot growth in commercial wood species. Antisense constructs of the nucleic acids can also be used to transform plants to reduce the expression of GA 2-oxidase (claimed) to promote plant growth, (e.g., to improve skin texture and fruit shape in apples, increase stem clearly and therefore yield in sugar cane, increase stem clearly and thubarb, improve malting yields and quality in cereals (particularly barley), and increase growth in woody species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATGGCACTTGGGTTTCAGTCCCACCTGATCATCTTTCATCATGTTGGTGAC 738
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Pred. No. 1.6e-125;
0; Mismatches 291; Indels 3;
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Best Local Similarity 67.5%;
Matches 612; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                        TGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAGCTGATAATAGGCTTGCCCCTTTC 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated plant gibberellin 2-oxidase enzymes and nucleic acids, used to produce transgenic plants with improved or altered growth characteristics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents cDNA encoding an Arabidopsis thaliana gibberellin (GA) 2-oxidase, PcGA2ox2. This enzyme is a GA 2-beta-hydroxylase that acts on C19-GAs and for which 2-beta-hydroxylation is its only activity. Hydroxylation at the 2-beta position of a GA results in a biologically inactive product, and is the most important route for GA metabolism in plants, ensuring that the active hormones do not
                                                                                                                                                      GCTCTTCAGGTTATGACTAACGGGAGGTTCAAGAGTGTTAAACACAGGGTCTTAGCCGAT
                                                                                                                    GCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTGTAAAAGCATAGGGTTTTGGCTGAC
                                                                                                                                                                                                                     ACAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACCAGCGTTGAGTGAAAATATA
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                                                                 GCACCTTTACCTTCAGTGATGTTAAAAGGAGAGAGTGTTTGTACAAAGAGTTCACATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "Gibberellin 2-oxidase AtGA2ox2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana gibberellin 2-oxidase AtGA2ox2 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ55916 standard; cDNA; 1237
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98GB-00015404
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CC TAINTY, 4-dilynoxoxy, 2-Dutannon-4-phosphate synthase actorized popuration as a cerombinant DNA construct comprising the polynucleotide, a cell with the comprising the polynucleotide operably linked to a tell asst one regalatory sequence, transforming a cell with the polynucleotide, a cell comprising the recombinant DNA construct, polynucleotide, a cell comprising the recombinant DNA construct and a seed comprising the recombinant DNA construct. Also disclosed as new are nucleic acid fragments and assembled contige encoding plant metabolism proteins chosen from GTP cyclohydrolase Ili3,4-dihydroxy-2-buttanone-4-phosphate CC sactor, Acyl-CoA thioceterase II,3,4-dihydroxy-2-buttanone-4-phosphate CC sound. The polypoptides are present at higher or lower levels than normally cell types or in developmental stages in which they are not normally CC pulymorphism (RELP). It can also be used to probe Southern blots containing restriction endonuclease-treated genomic DNAs of a set of individuals representing parent and progeny of a defined genetic acid fragment may be used to probe Southern blots against PCR amplification products generated from the mutation tag sequence profuce polyclonal or monoclonal antibodies with 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ACGCCCTTGTTCACGGGGATTCCTGTGGTCGACCTCACGCACCCCGATGCCAAGAATCTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 ACCAAATTTTCCTCAACAATTCCCATAGTGGACCTCTCCAAACCTGATGCAAAGACCCTT 278
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larity 65.7%; Pred. No. 1.66
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ACAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACCAGCGTTGAGTGAAAATATA 858
                                                                                                                                                                                          ACAAGGAGATCGAGGATTTCAATGATATTTTCGGCGGACCGCCATTGAGCCAGAAGATC 975
                                                                                                                                                                                                                                                                                                                                                                                                                   TGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAGCTGATAATAGGCTTGCCCCTTTC 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthase nucleic acid and proteins, useful for creating transgenic plants where polypeptides are present at higher or lower levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate
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Lohman KN, Rendina AR, Sakai H, Weng Z, Caimi PG, Fang Y;
Zoughi IL, Anderson SL, Shi J, Lu G, Helentjaris TG;
                                                                                                                                                                                                                                                                   GCACCTTTACCTTCAGTGATGTTAAAAGGAGAGAGTGTTTGTACAAAGAGTTCACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate synthase; Dioxygenses: Ent-Kautene Synthase A; GA-20 oxidase; Globerellin 3-beta hydroxylase; Riboflavin specific deaminase; Ethylene response factor; Acyl-CoA thioesterase II; ABC transporter GCN30-like; P-glycoprotein I; P-glycoprotein 3; P-glycoprotein B-glycoprotein HWMD12; ABC transporter; PMG TRAPGP; P-glycoprotein HWMD12; ABC transporter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated polynucleotide comprising a nucleotide sequence encoding a polypeptide having GTP cyclohydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; SEQ ID NO 13; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Soybean; 88; plant; plant metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DU PONT DE NEMOURS & CO E I.
PIONEER HI-BRED INT INC.
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99US-0143412P.
99US-014650P.
99US-0170906P.
99US-0172959P.
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30-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lee J, Lc
Shen JB,
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                                                                                                                799
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DB 12; Length 1352;

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I, Kinney AJ, Rafalski JA, Orozco EM, Miao G, Famodu OO; Lohman KN, Rendina AR, Sakai H, Weng Z, Caimi PG, Fang Y; Zoughi IL, Anderson SL, Shi J, Lu G, Helentjaris TG;

Allen SM, Lee J, Lo Shen JB, Li CP;

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987 CCTTTGAGTGAGAAAATAGCACCATTATCCTCTCTCTCATG---AAAGGAAAAGAAAGTCTA 1043
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ADM94205 standard; cDNA; 1365 Soybean Dioxygenase cDNA #1. (first entry) 17-JUN-2004 ADM94205;

Soybean; 88; plant; plant metabolism; GTP cyclohydrolase II/3, 4-dihydroxy-2-butanone-4-phosphate synthase; Dioxygenase; Ent-Kaurene Synthase A; GA-20 oxidase; didborrellin 3-beta hydroxylase; Riboflavin specific deaminase; Ethylene response factor; Acyl-CoA thioesterase II; ARC transporter GNA20-11ke; P-glycoprotein I; P-glycoprotein 3; P-glycoprotein PPGP; P-glycoprotein HWMD2; ARC transporter; PMP70 ARC transporter;

Glycine max.

US6677502-B1

13-JAN-2004.

2000US-00614912 12-JUL-2000;

12-JUL-1999

99US-0143401P. 99US-0143412P. 99US-0146650P. 99US-0170906P 99US-0172959P 15-DEC-1999; 21-DEC-1999; 21-DEC-1999; 12-JUL-1999 30-JUL-1999

DE NEMOURS & CO E I. HI-BRED INT INC. DU PONT (PION-)

The invention relates to an isolated polymuclectide comprising a muclectide sequence encoding a polypeptide having GTP cyclohydrchase cut activity, appearing as nuclectide sequence encoding a polypeptide having GTP cyclohydrclase [11/3,4-dihydrcxy-2-butanone-4-phosphate synthase activity, appearing as a LADM94266. Also included are a vector comprising the polymuclectide operably linked concentrate comprising the polymuclectide operably linked to at least one regulatory sequence, transforming a cell with the comprising transforming a plant cell with the polymuclectide and regenerating a plant from the transformed plant cell), producing a plant (comprising transforming a plant cell with the colymuclectide and regenerating a plant from the transformed plant cell). The polymuclectide and regenerating a plant from the transformed plant cell), the recombinant DNA construct and a seed comprising the recombinant DNA construct and a seed comprising the recombinant DNA construct and a seed comprising che plant seed in the construction of the polymorter and a seed comprising plants where containing can be used to create transgenic plants where for the polymorter in developmental stages in which they are not normally cell types or in developmental stages in which they are not normally collymorphisms (RFDP). It can also be used to probe Southern Diote containing restriction endomuclease-treated genomic DNAs of a set of individuals representing parent and progeny of a defined genetic cross containing restriction and progeny of a defined genetic cross containing restriction and product genome such sequence primer in continuing centuring parent and progeny of a defined genetic cross capaner primer in continuing the mutation and sequence primer in containing the polymorpac New isolated GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate synthase nucleic acid and proteins, useful for creating transgenic plants where polypeptides are present at higher or lower levels. Example 3; SEQ ID NO 5; 186pp; English. 2004-088430/09 P-PSDB; ADM94206. Eragment).

Sequence 1365 BP; 448 A; 258 C; 244 G; 415 T; 0 U; 0 Other;

7 285 180 61 ACGCCCTTGTTCACGGGGATTCCTGTGGTCGACCTCACGCACCCCCGATGCCAAGAATCTC 120 166 Argererrerrerekadeakacaka karaka 125 Argerekarakan 125 Argereka 155 9 1 ATGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAAACCATTCAAGTCC 226 ACCAAATTTTCCTCAACAATTCCCATAGTGGACCTCTCCAAACCTGATGCAAAGACCCTT 121 ATAGTGAACGCCTGTAGGGACTTCGCCTTCTTCAAGCTTGTGAACCATGGTGTTCCATTG Gaps Score 419.8; DB 12; Length 1365; Pred. No. 5.2e-124; 0; Mismatches 327; Indels 15; Query Match 42.1%; Best Local Similarity 65.6%; Matches 651; Conservative a 쉽 ò ઠે ò

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286 ATAGTGAAGGCTTGTGAGGAGTTTGGATTCTTCAAAGTCATCATCATGGTGTCTCCATG

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/*tag= a /product= "gibberellic acid 2-oxidase 2"

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The present sequence encodes a gibberellic acid 2-oxidase 2 protein describes which is used in the method of the invention. The specification describes methods for the inhibition and control of gibberellic acid levels. Gibberellic acid levels achievels. Gibberellic acid levels achievels. Gibberellic acid levels may be inhibited or controlled by use of a chimeric expression construct expressing a RNA or protein which suppresses the gibberellin biosynthetic pathway sequence, diverts substrate from the pathway, or degrades pathway substrates or products. The methods uses copalyl diphosphate synthase, 3beta-hydroxylase, 2-oxidase, phytoene synthase, C-20 oxidase, and a 2beta, 3beta-hydroxylase polymuclectides to achieve this. The method is used to control seed germination and seedling growth especially to regulate gene products of germination, in transgenic plants and restoration of normal seed germination, in transgenic plants produced are gibberellin deficient, and have shortened hypocotyl and/or epicotyl phenotypes
                                                                                                                                                                                                                                                                                                                                                                                                                                   Obtaining transgenic plant useful for controlling seed germination and seedling growth comprises transgene comprising a sequence expressing altered levels of an essential hormone.
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P-PSDB; AAY84100.
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03-JUL-2000

AAZ99472;

AA299472

RESULT

Glycine max

448

503

240

'n,

18;

Indels

. Match 42.0%; Score 418.2; DB 3; Local Similarity 66.2%; Pred. No. 1.7e-123; les 657; Conservative 0; Mismatches 318;

Length 1403;

208

SJ;

Loguech

Logusch EW,

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The invention relates to control of gibberellin (GA) levels in plants. The method involves producing transpenic plants having a phenotype of reduced seed germination and reduced early seedling growth, then restoring seed germination and early seedling growth by treating plants with an appropriate compound when conditions are favourable. The method is useful to control seed germination and/or early seedling growth in agricultural production so that unfavorable environmental conditions normally reducing agronomic output can be avoided and yields increased. Plants also demonstrate increased uniformity of germination, emergence and seedling vigor, so increasing yields at harvest. The method is especially useful in crop plants such as e.g. canola, soybean, cotton, cetc., and is also useful in storage and transport of seeds to reduce premanation which may affect a gronomic or food quality of the seeds. The present sequence is soybean GA 2-oxidase 2 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGITGAACCACIACCGCCTIGCCCTGAGGGACTGAACCGGAATTIGGITGGG 600
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                                                                                                       Control of gibberellin levels in plants useful to avoid unfavorable conditions in crops to increase yields, using transgenic plants having reduced seed germination and early seedling growth then treatment to restore these properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAAACCATTCAAGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 418.2; DB 6; Length 1403;
Pred. No. 1.7e-123;
0; Mismatches 318; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1403 BP; 440 A; 269 C; 261 G; 433 T; 0 U; 0 Other;
                 Kishore GM,
                                                                                                                                                                                   Claim 45; Page 94-95; 155pp; English
                 Heck GR,
Ream JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 42.0%;
Local Similarity 66.2%;
les 657; Conservative C
                 Blich TD,
                                                            2002-489107/52
                                  Rao S,
                                                                            P-PSDB; AAE24922
                  Brown SM,
Piller KJ,
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                                                                                                                                    AGGGTGAATCACTACCCTGCTTGCCCTGAACTT---GTGAATGGTCAAAACATGATAGGG
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                                              ATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTGATGCCGGAGGGGTTGCGG
                                                                           557 ATGTCTTCTGTGAGGAAAATGGCATGTGAGATTCTTGAGCTGATGGCAGAAGGATTGAAG
                                                                                                       ATAAGGCAGAGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGATTCGTGCTTC
                                                                                                                                                                  TTTGGGGAGCACACACACACACACATAATTTCTGTCTTAAGATCTAACAGCACATCTGGC
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The sequence that acts on C19-GAs and for which 2-beta-hydroxylation is hydroxylase that acts on C19-GAs and for which 2-beta-hydroxylation is the only activity. Hydroxylation at the 2-beta position of a GA results in a biologically inactive product, and is the most important route for GA metabolism in plants, ensuring that the active hormones do not accumulate in plants, ensuring that the active hormones do not accumulate in plants, ensuring that the active hormones do not accumulate in plant sensor in a biologically inactive product, and is the most important route for GA metabolism in plants, ensuring that the active hormones do not accumulate in plant sensor in a constitutively over-expressed or otherwise enhanced to reduce the concentration of bloactive GAs in the plants and therefore to inhibit plant growth. Growth inhibition is useful in many agricultural and horticultural applications such as enhancing cordinary and increasing yields (by the diversion of assimilates from cordinary and increasing yields (by the diversion of assimilates from infection, and increasing yields (by the diversion of assimilates from vegetative to reproductive organs). The nucleic acids may also be used to infection, and increasing yields (by expression in floral organs), cortain and and south in seedless grapes, citrus fruits and the nucleic acids can also be used to transform plants to reduce the expression of GA 2-oxidase (claimed) to promote plant growth, (e.g., to improve fruit set and growth in seedless grapes, citrus fruits and constructs of improve fruit set and growth in seedless grapes, citrus fruits and constructs of improve fruit set and growth in seedless grapes, inapprove skin texture and fruit shape in apples, increase stem central inhubarb, improve malting yields and quality in cereals increase growth in woody species
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  sequence represents cDNA encoding an Arabidopsis thaliana
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                                                             TITGGAGAACACAGGACCCACAAATCATITCTCTACTTAGGTCCAACAATACTTCAGGC
677 AGGGTGAATCACTACCCTGCTTGCCCTGAACTT---GTGAATGGTCAAAACATGGTAGGG
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                                                        ,, καιαιεκι υΑ, Οrozco ΕΜ, Μίαο G, Famodu ΟΟ,
Rendina AR, Sakai H, Weng Z, Caimi PG, Fang Y;
, Anderson SL, Shi J, Lu G, Helentjaris TG;
                                                                                                                                                                                              ACAAAGAGGTCAAGGATATCGATGATCTACTTCGCAGGTCCTCTTTGAGCGAGAAGATT
                                                                                                                                                                                                                                                                                                                                                           TCTCAATACAAGTTATCTGCTTACAAACTAAGGCTTGGTGACTATAGGCTTGGTCTCTTT
                  GATGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCCTTTTTCATCATGTTGGTGAC
                                                                                               GCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTGTAAAGGCATAGGGTTTTGGCTGAC
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                                                                                                                                                                                                                                                                                                                                TGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAGCTGATAATAGGCTTGCCCCTTTC
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                                                                                                                                                                                                                                                       GCACCTTTACCTTCAGTGATGTTAAAAGGAGAGAGTGTTTGTACAAAGAGTTCACATGG
                                                                                                                                                                                                                                                                                        GCACCATTATCATGCCTTGTGCCAAAGCAAGATGATTGCCTTTATAATGAGTTTACTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate synthase, Dioxygenase, Ent-Kaurene Synthase A; GA-20 oxidase; Gibberellin 3-beta hydroxylase; Riboflavin specific deaminase; Ethylene response factor; Acyl-CoA thioesterase II; ABC transporter GCN20-like; P-glycoprotein I; P-glycoprotein 3; P-glycoprotein HVMDR2; ABC transporter; P-glycoprotein HVMDR2; ABC transporter; PMP70 ABC transporter;
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(PION-) PIONBER HI-BRED INT INC.
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99US-0170906P.
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Zoughi IL,
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P-PSDB; ADM94208.
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The invention relates to an isolated polynucleotide comprising a nucleotide sequence encoding a polypeptide having GTP cyclohydrolase IN13.4-dihydroxy-2-butanone-4-phosphate synthase activity, appearing as AND34366. Also included are a vector comprising the polynucleotide operably linked to at least one regulatory sequence, transforming a cell with the comprising the recombinant DNA construct.

Dolynucleotide, a cell comprising the recombinant DNA construct, producing a plant (comprising the recombinant DNA construct, oplynucleotide operably linked to a plant comprising transforming a plant cell with the polynucleotide and regenerating a plant from the transformed plant cell), consent from GTP cyclohydrolase IN13.4-dihydroxy-2-butanone-4-phosphate comprising the recombinant DNA construct and a seed comprising the recombinant DNA construct and a seed comprising the recombinant DNA construct and a seed comprising che recombinant DNA construct and seed comprising the recombinant DNA construct and a seed comprising the recombinant DNA construct and a seed comprising ches recombinant DNA construct and a seed comprising the recombinant DNA construct and a seed comprising chessen, block of thiosesterase IN13.4-dihydroxy-2-butanone-4-phosphate chessen from GTP cyclohydroxy-2-butanone-4-phosphate chessen from GTP cyclohydroxy-3-beta hydroxy-3-beta hydroxy-3-
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where polypeptides are present at higher or lower levels
                                                                              Example 3; SEQ ID NO 7; 186pp; English.
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                                                                                                                                                                                                                                                                                                         ACAAAGAGTTCACATGGTGTGAATACAAGAGGCTGCGTACACTTCAAGGCTAGCTGATA 961
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                                                                                                 ATAGGGTTTTGGCTGACACAAGTCAAGGTTATCAATGATCTACTTTGGAGGACCAG
488 CCTGCGCCGTCCCGTCCTGCG------CGCTCTTCCGGGCGGCGCTGAACGAGTACA
                                  TAAGGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAAAAAGTGATTCGTGCTTCA
                                                                                                                                                                                                TCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTGTAAAGC
                TTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTGATGGCGGAGGGGGTTGGGGA
                                                                                       TTGGGGAGCACACACACACACACACACATTTCTGTCTTAAGATCTAACAGCACATCTGGCT
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09-MAR-1999;
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or otherwise enhanced to reduce the concentration of bloactive GAs in the plants and therefore to inhibit plant growth. Growth inhibition is useful many agricultural and horticultural applications such as enhancing lodging-resistance and grain yield in cereals, improving seedling callity, reducing the growth of amenity grasses, reducing shoot growth in creat and ornamental trees, improving tolerance to cold, drought and infection, and increasing yields (by the diversion of assimilates from vegetative to reproductive organs). The nucleic acids may also be used to induce male and/or female sterility (by expression in floral organs), prevent per-harvest sprouting, reduce shoot growth in commercial wood species. Antisense constructs of reduce shoot growth in commercial wood species. Antisense constructs of the nucleic acids can also be used to transform plants to reduce the expression of GA 2-oxidase (claimed) to promote plant growth, (e.g., to improve fruit set and growth in seedless grapes, citrus fruits and learn and therefore yield in sugar cane, increase stem length and therefore yield in sugar cane, increase yield and earliness in celery and rhubarb, improve malting yields and quality in cereals (particularly barley), and increase growth in woody species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             735 CCTTCTTCTTCAACGTTGGTGACTCTCTCCAGGTGATGACAAATGGGGAGGTTCAAGAGGC 794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 TGAAAGCATGCGAAGACTTCGCCTTCTTCAAGGTGATCAACCATGGCGTTTCCGCAGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 CCTTGTTCACGGGGATTCCTGTGGTCGACCTCACGCACCCCGATGCCAAGAATCTCATAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 TAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 ACAGAGCTGGTCCCCCCGACCCTTTCGGCTATGGTAGCAAGAGGATTGGCCCAAACGGTG
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Pred. No. 1.2e-103;
0; Mismatches 329;
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Matches 586; Conservative
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                                                                                 CCTTTTTCATCATGATGGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTTTGTACAAAGAGTTCACATGGTGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAG
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              CCTTCTTCTTCAACGTTGGTGACTCTCCCAGGTGATGACAAATGGGAGGTTCAAGAGCG
                                                                                                                                                                                                                                TAAAGCATAGGGTTTTTGGCTGACACAACGAAGTCAAGGTTATCAATGATCTACTTTGGAG
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/product= "Gibberellin 2-oxidase AtGA2ox1"
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BW685035 BP074757

BP074168 EA27D12a GA Ed007

Minimum DB Maximum DB B

Database

Searched:

Sequence:

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Run

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Shoemaker, R. Kein, P., Vodkin, L., Erpelding, J., Coryell, V., Shoemaker, R., Kein, P., Vodkin, L., Erpelding, J., Coryell, V., Kanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., Public Soybean EST Project
Unpublished (1999)
Other_ESTS: BU544870 corresponding to Gm-r1088-979 (3')
Other_ESTS: BU544870 corresponding to Gm-r1088-979 (3')
Public Soybean EST Project
Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: B133 4163; email: info@biogeneticservices.com)
Insert Length: 1472 Std Error: 0.00
High quality sequence stop: 436.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                           CV292717
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BBC074158
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CA844443
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Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kudsha, T., Martin, J.,
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Schurk, R., Waterston, R. and Wilson, R.,
McCann, R., Waterston, R. and Wilson, R.,
Dublic Soybean EST Project
Unjublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Porset Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estGwatson, wustl.edu
When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Blogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
High quality sequence stop: 1656
Glycine max Glycine max Buraryota, Embryophyta; Tracheophyta; Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                      ORGANISM
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AUTHORS
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JOURNAL
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                                               /done lib="Gm-c1023"
//done lib="Gm-c1023"
//done lib="Gm-c1023"
//note="Vector: pSPORT1; Site_1: Sal1; Site_2: NotI; This cDNA library was constructed from mRNA isolated from seed coats (100-200mgs) of greenhouse grown plants. The library was prepared using the Life Technologies pSuperScript cDNA library construction kit. Complimentary DNA was synthesized from mRNA using a poly (dT) sequence with a Not I restrictions site. Sal I linkers adapers were ligated to the blunt-ended cDNA fragments followed by Not I digestion. The CDNA fragments were directionally cloned into the Not I -Sal I restriction site of the pSPORTI vector. The ligated cDNA fragments were transformed into E.coli Electromax DH10B host cells. This library was constructed by Dr. Lila Vodkin and Dr. Anu Khanna."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 ACGCCTTGTTCGCGGGGATTCCTGTGGTCGACCTCACGGACCCCGGATGCCAAGACCCA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 AAAGACAGAGCTGGTCCCCCCGACCCTTTCGGCTATGGTAGCAAGAGGATTGGCCCAAAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            384 GGCGATGTCGGTTGGGTCGGATACCTCCTTCTCAACACCAACCCTGATGTCATCTCCCCCC 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 ATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTGATGGCGGAGGGGTTGGGG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATAAGGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGATTCGTGCTTC 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATAGTGAACGCCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCCATTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 ATAGTCAATGCCTGCAGGGACTTCGGCTTCTTCAAGCTCGTGAACCACGGTGTTCCGTTA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 CAGTICATGGCCAATITGGAAAACGAAACCTCGGGTICTTCAAAAAACCTCAATCCGAG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324 AAAGACAGGGCTGGTCCCCCTGACCCTTTTGGCTACGGCAGGAGGAGGATTGGCCCTAAC 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 GGTGATGTCGGTTGGGTCGAATACCTCCTCAACACCCAACCCTGATGTTATCTCACCC 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGGTTGTTGTGTGTGAGCATTGAACAGTTTTTCCTTCTGAAACCATTCAAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 GAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  504 ATTAGAGCGGTGAAGAACATGTGCTATGAGGTGTTGGAATTGATGGCTGANGGATTGTGG
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     'tissue_type="seed coats of greenhouse grown plants'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 454; DB 1; Length 653;
Pred. No. 1.8e-127;
0; Mismatches 73; Indels
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Best Local Similarity 87.2%;
Matches 496; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 GAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG 240
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al Similarity 88.0%; Pred. No. 3.1e-124;
483; Conservative 0; Mismatches 66;
1. .566
/organism="Glycine max"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 483; Conserv
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BM085298 53-JUL-2004 ag) 4407.yl Gm-c1066 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1066-4957 5' similar to TR:Q9XG83 Q9XG83 GA 2-OXIDASE. ;, mRNA

DEFINITION

GI:16995926

BM085298.1 EST. seguence

ACCESSION VERSION KEYWORDS

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TGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAGCTGATAATAGGCTTGCCCCTTTC 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGAGAAAATCCTCATCATTTCAGGGGGGGGGGGAGAACTACATTACAGCAGTGAAGAAC 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                439 ATGTGCTATGCGGTGTTGGAATTGATGGCGGAGGGGTTGGGGATAAGGCAGAGAATAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTGTAAAGCATAGGGTTTTGGCTGAC 798
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              /tissue_type="Flowers and
/ecotype="Col-0"
/plasmid="pCMVSPORT_6"
clone="GSLTFB7ZE01"
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Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.

Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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(Dasse 1 to 1355)
Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNSOAC6N 1165 bp mRNA linear HTC 06-FEB-2004 Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTFB7ZE01 of Flowers and buds of strain col-0 of Arabidopsis
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
 257
                                                    AAAGACAGGCTGGTCCCCCTGATCTTTTGGCTACGCAGCAAGAAGAAGATTGGCCTAAC
                                                                                                                     ATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTGATGGCGGAGGGGTTTGGGG
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Location/Qualifiers
 GAGTTCATGGCCAATTTGGAAAACGAAACCCTCAGGTTCTTCAAAAAACCTCAGTCCGAC
                                                                                                                                                                        AAATCACTTTGCATTTTCCGAGAAAATCCTCATCATTTCAGGGCGGTGGTGGAGAACTAC
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetler, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
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HTC; GSLT CDNA.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

UKGV INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
Menard,M., Craud,C., Quetier,F., Scarpelli,C., Schachter,V.,
Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                             Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTPGH782H09 of Hormone Treated Callus of strain col-0 of
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HTCh GSLT cDNA.
Arabidopsis thaliana (thale cress)
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; cosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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/db_xref="taxon:3702"
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/mol_type="mRNA"
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Unpublished Corresponding to Gm-c1065-2970 (5')
Conter ESTS BG881784 corresponding to Gm-c1065-2970 (5')
Soybean (NSF 9872565)
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Swhn R. Madigan Bullding, 1201 W. Gregory, Urbana, IL 61801, USA
Tel: (217) 244-6147
Fax: (217) 333-4582
                                                                                                                                                                         ACAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACCAGCGTTGAGTGAAATATA
                                                 CCACAGATAATTTCTGTCTTAAGATCTAACAGCACATCTGGCTTGCAAATCTGTCTCACA
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Insert Length: 622 Std Error: 0.00
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gag primer: 5'-TTTTTTTTTTTTTTTTTT (A/C/G)-3'
High quality sequence stop: 622.
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Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
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URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
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       Combined Approach to Evaluate and Improve Arabidopsis Genome
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    1141
    organism="Arabidopsis thaliana"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue type="Flowers and buds"
/ecotype="Col-0"
/plasmid="pCMVSPORT_6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:3702"
/clone="GSLTFB20ZE08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l. .1141
/gene="At1g30040"
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set of 9,216 low redundancy clones selected from CDNA libraries from various fissues and stages of development of soybean that consists of 2,706 CDNAs from germinating cotyledons (source library Gm-c1027); 1,355 CDNAS from immature seed coats (libraries Gm-c1019 and Gm-c1023); 917 CDNAs from tissue culture derived somatic embryos (source libraries Gm-c1019); 3,275 CDNAs from germinating seedlings, shoot tips, or leaves exposed to various stresses (source libraries Gm-c1064, Gm-c1065, Gm-c1066, and Gm-c1067; and Gm-c1068); and 963 CDNAs from young leaves exposed to bacterial and fungal pathogens (source libraries Gm-c1072, Gm-c1073, and Gm-c1074). The 5' ESTS of the source clones from the different libraries was used to select singletons, or a representative of each contig, which were reracked to form library Gm-c1089 and the CDNA clones of the reracked Gm-r1088 library were then sequencing was funded by NSF Plant Genome project #8872565 (http://soybeangenomics.cropsci.uiuc.edu/) as part of creation of a low redundancy soybean CDNA set. The source CDNA libraries were constructed by the laboratories of Lila vodkin, University of Illinois, Randy Shoemaker, Iowa State University, and Paul Keim, Notrhern Arizona University as part of the Public EST project, thtp://lso.186.26.94/soybeanset.html. The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Center for Computational Genomics and Bloinformatics, University of Minnesota, http://web.ahc.umn.edu/biodata/nsfsoy/. Reracking and 3' sequencing were conducted by services of the University of Illinois Keck Center for Computational Genomics http://web.ahc.umn.edu/biodata/nsfsoy/. Reracking and 3' sequencing were conducted by services of the University of Illinois Seck Center for Computational Genomics http://web.ahc.um.edu/biodata/nsc.um.edu/keck.htm. Note: The corresponding 5' EST from each clone in the Gurne library for each clone can also be obtained by referring to the Genome Systems clone clone in the cource library for each cl
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                                                                                                                                                                                                                                                                                                                                                                                                                          723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCAATGTTGGTGACACTCTACAGGTGATGACTAATGGGAGGTTTAAAAGTGTAAAGCAT 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGGTTTTGGCTGACAAAGTCAAGGTTATCAATGATCTACTTTGGAGGACCAGCG 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321 AGAGITITIGGCIGACCCAACCAAGICAAGGITGICAAIGAICTACITIGGAGGAGGACCCC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGAGTGAAAATATAGCACCTTTACCTTCAGTGATGTTAAAAGGAGAGGAGTGTTTGTAC 903
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                                                                                                                                                                                                                 AACCACTACCCGCCTTGCCCTGAGGTGCAAGCACTGAA----CCGGAATTTGGTTGGTTT
                                                                                                                                                                                                                                                                                                                     GGGGAGCACACACACACACACACATTTCTGTCTTAAGATCTAACAGCACATCTGGCTTG
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                                                           Gaps
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Score 420.4; DB 5; Length 622;
Pred. No. 3.7e-117;
0; Mismatches 49; Indels 3.
  tch 42.2%; al Similarity 89.9%; 461; Conservative
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                                Best Local
Matches 46
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Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G. Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M. Want Cruaud C., Annotation is based on the Mulich Information center for Protein Sequences): 5 prime and 3 prime are assembled with Phrap.
                                                                                                                                                                                                                                                                                    CNSOABKL 1363 bp mRNA linear HTC 06-FEB-2004 Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTPGH20ZC07 of Hormone Treated Callus of strain col-0 of Arabidopsis thaliana (thale cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetler, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
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201 AAAGAATTCACATGGTGGGAATACAAGAAGGCTGCGTAATGCGTCAAGGCTAGCGGATAAT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                   BX815974.1 GI:42471555
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta; eudicotyledons, core eudicotyledons, rosids II, Brassicales, Brassicaceae, Arabidopsis.
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Location/Qualifiers
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/ecotype="Col-0"
/plasmid="pCMVSPORT_6"
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                                                                                                                                                 141 AGGCTCGCTCCTTTTGAGAATCTGCTGCTGAT 109
                                                                                         964 AGGCTTGCCCCTTTCCAGAAATCTGCTGCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="GSLTPGH20ZC07"
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/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                        DEFINITION
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Direct Submission

Direct Submission

Direct Submission

Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librarises construction : Temple G.

Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGV INRA : Clepet C., Caboche M. 2003 version of the Arabidopsis Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

Liength, Length.
Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weisenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
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Location/Qualifiers
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    1339
/organism="Arabidopsis thaliana"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon.3702"
/clone="GSLYFB702F11"
/tissue_type="Flowers and bu /ecotype="Col-0"
/plasmid="pcMVSPORT_6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="At1g30040"
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           AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTFB70ZF11 of Flowers and buds of strain col-0 of Arabidopsis thaliana (thale cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   970 GCACCATTGCCATGCCTTGTCCCTGAGCAAGATGATTGGCTTTACAAAGAATTCACTTGG 1029
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HTC; GSLT CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATGGCACTTGGGTTTCAGTCCCACCTGATCAGACTTCCTTTTTCATCAATGTTGGTGAC 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCACCTTTACCTTCAGTGATGTTAAAAGGAGGAGTGTTTGTACAAAGAGTTCACATGG
                                                                                                                                                                      ccreaacceracecrratecraaraaccearresaccaaaccereaccrreerresarr
                                                                                                                                                                                                                                                              433 TAGTATCTCCTCCTCAATGCTAATCCTCAGCTCTCCTCTCCTAAAACCTCCGCCGTTTTC
                                                                                                                                                                                                                                                                                                           CGAGAAAATCCTCATCATTTCAGGGGGGGTGGTGGAGAACTACATTACAGCAGTGAAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTAAGCAGGTTGCTGAAGGATGAGAAAAGTGATTCGTGCTTCAGGTTGAACCACTACCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGCAGGAGGCTATTGGCTTCTTGGCCTCAGTCTCTTAAAAACCGGGCCGGTCCA
                                                                                                                           CCCGACCCTTTCGGCTATGGTAGCAAGAGGATTGGCCCAAACGGTGATGTCGGTTGGGTC
                                                                                                                                                                                                                     GAATACCTCCTCAACACCCAACCCTGATGTTATCTCACCCAAATCACTTTGCATTTTC
                                                                                                                                                                                                                                                                                                                                                                                                     ATGTGCTATGCGGTGTTGGAATTGATGGCGGAGGGGTTGGGGGATAAGGCAGAAGAATACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                GTTTCGTACAAGGTGTTGGAGATGGTTGCCGAAGAACTAGGGGATAGAGCCAAGGGACACT
                                   GAAAACGAGGCCCTCAGGTTCTTTAAAAATCTCAGTCCGAGAAAGACAGAGCTGGTCCC
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AJ803092 Antirrhinum majus whole plant Antirrhinum majus cDNA clone 018 5 05 018, mRNA sequence.
AJ803092 Antirrhinum majus whole plant Antirrhinum majus cDNA clone AJ803092. 
EST.
                                                                                                   /note="Vector: pBluescript II SK+, Site 1: EcoRI, Site 2: XhoI; The cDNA library was constructed from floral meristematic mRNA provided by Dr. Halina Knap of Clemson University. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The
                                                                                                                                                                                                                                                                                     cDNA fragments were directionally cloned into the ECORI-XhoI restriction site of the pBluescript vector. The injacted cDNA fragments were transformed into DH10B host cells (GibcoBRI). This library was constructed in the laboratory of Dr. Randy Shoemaker."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 ATAGTGAACGCCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCCATTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ACGCCCTTGTTCACGGGGATTCCTGTGGTCGACCTCACGCACCCCGATGCCAAGAATCTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271 ATAGICAAIGCCIGCAGGGACTICGGCTICTICAAGCICGIGAACCACGGIGTICCGTIA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      391 AAAGACAGGCCTGGTCCCCCTGACCCTTTTGGCTACGCCAGCAAGAGGATTGGCCCTAAC 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiids; Lamiales; Plantaginaceae; Antirrhineae;
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1 (bases 1 to 785)

Bey,M., Stueber,K., Fellenberg,K., Schwarz-Sommer,Z., Sommer,H., Saedler,H. and Zachgo,S.
Characterization of Antirrhinum Petal Development and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 ACGCCCTTGTTCGCGGGGATTCCTGTGGTCGACCTCACGGACCCCGATGCCAAGACCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331 CAGTICATGGCCAATTIGGAAAACGAAACCTCGGGTTCTTCAAAAAACCTCAATCCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTGATGTCGGTTGGGTCGAATACCTCCTCCAACACCAACCTGATGTTATCTCACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 AAATCACTTTGCATTTTCCGAGAAAATCCTCATCATTTCAGGGCGGTGGTGGAGAACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          511 AAGTCACAGTTCATTTTCAGAGAACGTCCTCAGAATTTCATGGCGGTGGTGGAGGAATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAAACCATTCAAGTCC
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     clone="GENOME SYSTEMS CLONE ID: Gm-c1051-1097"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 612;
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                          /tissue_type="floral meristematic mRNA"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             571 ATTAGAGCGGTGAAACACATGTGCTATGACGTGGTGGAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.7%; Score 375.6; DB 2;
88.3%; Pred. No. 2.1e-103;
ive 0; Mismatches 54;
                                                                              /clone_lib="Gm-c1051"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antirrhinum majus (snapdragon)
Antirrhinum majus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 408; Conserv
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Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, M.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             970 GCACCATTGCCATTGCCTTGTCCCTGAGCAAGATGGTTTGTGCTTTACAAAGAATTCACT 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE802903 612-2004 sx46c09.yl Gm-c1051 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1051-1097 5' similar to TR:064692 064692 PUTATIVE GA4 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through. Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
High quality sequence stop: 413.
                                                                              CCACAGATAATTTCTGTCTTAAGATCTAACAGCACATCTGGCTTGCAAATCTGTCTCACA 678
                                                                                                                                                                                                       ccacadaraarcrcagrecraagarcraaraacaceeeeeerrcrcaaarcrereraaa 789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              910 ACAAGGAGATCGAGGATTTCAATGATATATTTCGGCGGACCGCCATTGAGCCAGAAGATC 969
  672
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CTGAGTAAAATGCTGAGAGATGAGAAGAGTGACTCGTGCCTGAGACTAAACCATTATCCG
                                                                                                                                                                                                                                                                                                             Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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/mol_type="mRNA"
/cultivar="Corolla"
/db_xref="taxon:3847"
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identification of Target Genes of the Class B MADS Box Gene
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                                                                                                                                                                          /organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="taxon:4151"
/clone="1018_5 05 018"
/tissue type="Whole plant"
/clone_lib="Antirrhinum majus whole plant"
                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 232; Indels
                                                                Contact: Schwarz-Sommer Z
Molekulare Pflanzengenetik
MPI fuer Zuechtungsforschung
Carl-von-Linne Weg 10, D-50829, Germany.
Location/Qualifiers
                                   Plant Cell 16 (12), 3197-3215
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Direct Submissions.

Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jailnon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M. WRW INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Mulich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
                                                                                                                                                                                         Arabidopsis thaliana (thale cress)
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana (thale cress)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.
Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                              06-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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                                                                   Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTFB56ZG10 of Flowers and buds of strain col-0 of Arabidopsis
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/organism="Arabidopsis thaliana"
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/ecctype="Col-0"
/plasmid="pcovySporr 6"
complement (1. .1128)
/gene="Atlg78440"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:3702"
/clone="GSLTFB56ZG10"
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                                                                                                                                             BX814091
BX814091.1 GI:42474058
                                                                                                                    thaliana (thale cress).
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2 (bases 1 to 1128)
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Direct Submission
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Matches 58
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DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
RESULT 11
CNSOADMT
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AUTHORS
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JOURNAL
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Anotes—Typector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Suspension cultures of L.esculentum E6203 were grown in Mursahige and Skoog based medium, supplemented with 15% coconut milk (filter sterilized and added after autoclaving), 2% saccharose, and lmg/ml 2,4D (pH5.8). Eresh medium was added every 7 days, and cultures were grown at 25 C, with 12hrs of light and continuous shaking."
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                     Email: http://www.genome.clemson.edu/orders/index.html
Location/Qualifiers
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                                                                            /organism="Lycopersicon esculentum"
/mol type="mRNA"
/culfivar="TA496, E6203"
/db xref="taxon:4081"
/clone="cTOS17020"
/tissume_type="suppension cultures"
/clone="SOE"
/clone_lib="GOE"
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    100 Jordan Hall, Clemson,
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Lycopersicon esculentum
Lycopersicon esculentum
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Spermatophyta; Jamids; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 694)
Van der Hoeven, R., Sun, H., Bezzerides, J., Cho, J., Utterback, R.,
Generation of Ests from Tomato Suspension Cultures
Unpublished (2001)
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Clemson University Genomics Institute
Clemson University
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BI208568
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337 GAGTTCATGGCCAATTTGGAAAAGGAAACCCTCAGGTTCTTCAAAAAACCTCAGTCCGAC 396
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To (bases 1 to 567)

Shoemaker, K. Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,

Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,

Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,

Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,

Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,

Public Soybean EST Project

Unpublished (1999)

Public Soybean EST Project

Contact: Shoemaker R/Public Soybean EST Project
                                                                      BM893076 567 bp mRNA linear EST 05-JUL-2004 sam51f05.yl Gm-c1069 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1069-2961 5' similar to TR:Q9XG83 Q9XG83 GA 2-OXIDASE. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Seq primer: -40RP from Gibco
High quality sequence stop: 435.
                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosida; eurosida I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/cultivar="williams"
/db xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1069-2961"
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/organism="Glycine max"
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                                                                                                                                                                          BM893076.1 GI:19348544
                                                                                                                                                                                                            Glycine max (soybean)
Glycine max
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                                        RESULT 13
                                                                                                                                                                                                                                                                                                                              REFERENCE
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                                                        BM893076
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followed libe "MtBC"

// Inote = "Vector: pBluescript pSK; Site 1: EcoRI; Site 2:

// Inote = "Vector: pBluescript pSK; Site 1: EcoRI; Site 2:

// Inote = "Vector: pBluescript pSK; Site 2:

// Inote = "Vector: pBluescript pSK; Site 2:

// Inote = Vector: pBluescript pSK; Site 3:

// Inote = Vector: pSK; S
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MCBG10E02F1 MCBC Medicago truncatula CDNA clone MtBC10E02 T3, mRNA
sequence.
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/dev_stage="harvested 3 weeks post inoculation with Glomus
intraradices"
                                                                                                                    456
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241 AAAGACAGAGCTGGTCCCCCCGACCCTTTCGGCTATGGTAGCAAGAGGATTGGCCCAAAC 300
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Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O., Niebel, A., Carreau, V., Charagnier, O., Kahn, D., Garreau, V., and Gamas, P. Medicago truncatula ESTs from endomycorrhizal roots Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Contact: Pascal Gamas and Etienne-Pascal Journet, Laboratoire
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email:
                                                                397 AAAGACAGGGCTGGTCCCCCTGATCCTTTTGGCTACGGCAGCAACGAGGATTGGCCCTAAC
                                                                                                                                                                                                                                                                                                                      457 GGGATGTGGGGTGGGTGGAATACCTCCTTCTCAACACCCAACCCTGACGTCATCTCCCCCC
                                                                                                                                                                                                                                               301 GGTGATGTCGGTTGGGTCGAATACCTCCTCCTCAACACCCAACCCTGATGTTATCTCACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 AAATCACTTTGCATTTTCCGAGAAAATCCTCATCATTTCAGGGCGGTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Medicago truncatula"
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Medicago truncatula
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/cultivar="Jemalong"
/db_xref="taxon:3880"
/clone="MtBC10E02"
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1 ATGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAAACCATTCAAGTCC

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47;

Score 334.8; DB 3 Pred. No. 6.9e-91; 0; Mismatches 47

33.6%;

Conservative

Matches 363; Query Match Best Local S

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Similarity

DB 3; Length 567; Indels

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/done_libe_Late Blight-challenged Tubers"
//note="Vector: pBluescript II SK(+) KR; Site 1: ECORI;
Site_2: Khoi; supplier: Pathogen-challenge series Tubers
Site_2: Khoi; supplier: Pathogen-challenge series Tubers
from pathogen-free Solanum tuberosum var. Shepody, clone
1756, were inoculated with 5 ul of Phytophthora infestans
(A2-mating type), through 2 puncture wounds 3 cm apart.
The tubers were inocubated 1 minute to allow inoculum
absorption. The infection area was outlined for future
collection reference. Surface slices were sampled from the
tubers at 1 day, 5 days, 7 days, 11 days and 14 days
post-infection. All samples were pooled and used for RNA
isolation and library construction. A normalized library
was constructed following a modified protocol of Bonaldo
et al. (1996. Genome Research 6: 791-806)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 GCTTGTGAGATTCTTGAAATGTTAGCAGGGATTAAAAATTCATCCAAAGAATGTATTT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 AGTAAGCTTTTAATGGATGAAAAAGTGATTCACTTTTTAGGCTAAATCATTACCCTCCA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACACAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACCAGCGTTGAGTGAAAAT 855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACCCTTTCGGCTATGGTAGCAAGAGGATTGGCCCAAACGGTGATGTCGGTTGGGTCGAA
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                                                          organism="Solanum tuberosum'
                                                                                                                                             /db_xref="taxon:4113"
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Location/Qualifiers
                                                                                  /mol_type="mRNA"
/cultivar="Shepody"
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1 (Dases 1 to 833)
Flinn, B., Rothwell, C., Sardana, R., Griffiths, R., Lague, M., De Koeyer, D., Audy, P., Goyer, C., Li, X.-Q., Wang-Pruski, G. and Regan, S. Unpublished (2005)
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                     RNA was extracted from whole root systems. CNNA was prepared from polyA+ enriched RNA. The CDNA was directionally ligated into Uni-zap KR vector from Stratagene and packaged using Gigapack Gold packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using Exhssit helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, Evry, France). Note: EST may be of
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921 College Hill Rd, Fredericton, ON, E3B 629, CANADA
Email: bflinn@bioatlantech.nb.ca
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'Cgn2_6/ptodata/1/ina/H_COMB.seq:*
'Cgn2_6/ptodata/1/ina/H_COMB.seq:*
'Cgn2_6/ptodata/1/ina/H_COMB.seq:*
'Cgn2_6/ptodata/1/ina/PE_COMB.seq:*
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'Cgn2_6/ptodata/1/ina/PE_COMB.seq:*
'Cgn2_6/ptodata/1/ina/RE_COMB.seq:*
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Listing first 45 summaries
                                                                                                                 - nucleic search, using sw model
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Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 6, Appli Sequence 6, Appli Sequence 5, Appli Sequence 12, Appli Sequence 12, Appli Sequence 13, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli		100.0%; Score 996; DB 3; Length 1318; ; Conservative 0; Mismatches 0; Indels 0; Gaps 0 ATGGTTGTTCTGTCTCAGCAGCATGAACCAGTTTTCCTTCTGAAACCATTCAAGTCC 60
US-08-823-986A-1 US-08-784-385-1 US-08-784-385-1 US-08-784-385-3 US-08-823-986A-3 US-09-371-307-69 US-09-373-666-13 US-09-614-912-41 US-09-614-912-41 US-09-614-912-43 US-09-614-912-43 US-09-614-912-43	n US/09719108 trephen G eter Andrew L Gibberellin 2-Oxidase 0.0970000 0.0970000 0.0990001 0.0990001 0.0990001 0.0990001 0.0987 0.090001 0.0987 0.090001 0.0987 0.090001 0.0990001 0.090001 0.090001	#; Score 996; DB 3; #; Pred. No. 0; 0; Mismatches 0 GCCAGCATTGAACCAGTTTTT
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                                                          Score 827.4; DB 3;
Pred. No. 3.5e-268;
1; Mismatches 97;
                                                            Query Match
Best Local Similarity 89.9%;
Matches 898; Conservative
           TYPE: DNA
ORGANISM: Glycine max
US-09-371-307-62
  LENGTH: 1359
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                                                   GGTGATGTCGGTTCGGTCGAATACCTCCTCTCAACACACCTGATGTTATCTCACCC
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Patent No. 6723897
GENERAL INFORMATION:
APPLICANT: Herow, Sherri M.
APPLICANT: Herow, Gregory R.
APPLICANT: Filler, Kenneth J.
APPLICANT: Elich, Tedd D.
APPLICANT: Elich, Tedd D.
APPLICANT: Logusch, Eugene W.
APPLICANT: Logusch, Eugene W.
APPLICANT: Logusch, Eugene W.
APPLICANT: Logusch, Sherry J.
APPLICANT: Logusch, Sherry J.
TITLE OF INVENTION: Methods for controlling gib.
FILE REFERENCE: MOBT:216
CURRENT APPLICATION NUMBER: US/09/371,307A
CURRENT FILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PATENTIN Ver. 2.0
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0; Mismatches 326;
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APPLICANT: Famodu, Omolayo O.
APPLICANT: Eamodu, Omolayo O.
APPLICANT: Sakai, Hajime
APPLICANT: Sakai, Hajime
APPLICANT: Weng, Zude
APPLICANT: Weng, Zude
APPLICANT: Caimi, Perry G
APPLICANT: Weng, Zude
APPLICANT: Danr Wetabolism Genes
FILE REFERENCE: BB1378 US, 09/614,912
CURRENT FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/146,650
PRIOR APPLICATION NUMBER: 60/146,650
PRIOR PILING DATE: 1999-07-30
PRIOR PILING DATE: 1999-12-15
PRIOR PLING DATE: 1999-12-21
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Patent No. 6677502
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Orozco, Buddy
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; ORGANISM: Glycine max
US-09-614-912-13
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Pred. No. 3.5e-132;
0; Mismatches 291;
             GATAATAGGCTTGCCCCTTTCCAGAAATCTGCTGCTGAT
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APPLICANT: Thomas, Stephen G
APPLICANT: Thomas, Stephen G
APPLICANT: Theden, Peter
APPLICANT: Hedden, Peter
TITLE OF INVENTION: Glaberellin 2-Oxidase
FILE REFERENCE: 0623.097000
CURRENT APPLICATION WUMBER: US/09/719,108
FRIOR FILING DATE: 1999-06-11
PRIOR FILING DATE: 1999-06-12
PRIOR FILING DATE: 1998-06-12
PRIOR PILING DATE: 1998-06-12
PRIOR PILING DATE: 1998-07-15
SPRIOR PILING DATE: 1998-07-15
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Patent No. 6670527
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APPLICANT: Safata, Hallme
APPLICANT: Caimi, Perry G
APPLICANT: Plant Metabolism Genes
FILE REFERENCE: BB1378 US NA (1906)
FILE REFERENCE: BB1378 US NA (1906)
FILE REFERENCE: BB1378 US NA (1906)
FRIOR APPLICATION NUMBER: 60/143,412
PRIOR FILING DATE: 1999-07-12
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: 60/170,906
PRIOR APPLICATION NUMBER: 60/172,959
PRIOR PILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/172,959
PRIOR PILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/172,946
PRIOR SEQ ID NOS: 204
NUMBER OF SEQ ID NOS: 204
                 Famodu, Omolayo O.
Lee, Jian Ming
Sakai, Hajime
Weng, Zude
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Best Local Similarity 65.6%;
Matches 651; Conservative (
 Miao, Gou-Hau
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ORGANISM: Glycine max
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                                                                                                                                            181 GAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG 240
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ACGCCCTTGTTCACGGGGATTCCTGTGGTCGACCTCACGCACCCCGATGCCAAGAATCTC 120
                                                                      121 ATAGTGAACGCCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCCATTG 180
                                                                                               339 GAAGCTATATCCGAATTGGAATATGAAGCCTTCAAATTCTTCTTCTTATGTCACTCAATGAA 398
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                            219 ACCAAATTTCCTCAACAATTCCCATAGTGGACCTCTCCAAACCTGATGCAAAGACCTT
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  Length 1365;
                                                    Indels
Score 419.8; DB 3;
Pred. No. 1.3e-130;
0; Mismatches 327;
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Sequence 5, Application US/09614912 Patent No. 6677502 GENERAL INFORMATION: APPLICANT: Allen, Steve APPLICANT: Rafalski, Antoni

RESULT 5 US-09-614-912-5

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TTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTGTAAAAG
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                                                                                                                                                                  TIGCAAAICTGICICACAGAIGGCACTIGGGITICAGICCCACCIGAICAGACTICCTIT
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APPLICANT: Brown, Sherri M.
APPLICANT: Heck, Gregory R.
APPLICANT: Filler, Kenneth J.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Bao, Sudabathula
APPLICANT: Logusch, Sherry J.
TTILE OF INVENTION: Methods for controlling gibberellin levels
FILE REFERENCE: MOBT:216
CURRENT APPLICATION WHERR: US/09/371,307A
CURRENT FILING DATE: 1999-08-10
NOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 64
LENGTH: 1403
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Pred. No. 4.7e-130;
0; Mismatches 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATAGACTTGAACATTTTGAAAGAATTGCAGCT 1143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.0%;
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   913 TCTCAATACAAGTTATCTGCTTACAAACTAAGCTTGGTGACTATAGGCTTGGTCTCTTT 972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 TGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAAACCATTCAAGTCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Miao, Gou-Hau
APPLICANT: Famodu, Omolayo O.
APPLICANT: Famodu, Omolayo O.
APPLICANT: Ee, Jian Ming
APPLICANT: Sakai, Hajime
APPLICANT: Sakai, Hajime
APPLICANT: Galmi, Perry G
APPLICANT: Anderson, Shawn
TITLE OF INVENTION: Plant Metabolism Genes
FILE REFERENCE: BB139 US NA
TITLE OF INVENTION: Plant Metabolism Genes
FILE REFERENCE: BB139 US NA
CURRENT APPLICATION NUMBER: US/09/614,912
CURRENT FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/143,412
PRIOR FILING DATE: 1999-07-12
PRIOR PILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: 60/170,906
PRIOR PILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: 60/172,959
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 204
NUMBER OF SEQ ID NOS: 204
NUMBER OF SEQ ID NOS: 204
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Patent No. 6677502
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                                                                                                                                                                                                                                                                                                                                                                                  Allen, Steve
Rafalski, Antoni
Orozco, Buddy
                                                                    979 CAGAAA 984
                                                                                                                               973 GAGAAA 978
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iive 0; Mismatches 314;
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: GB 9815404.0
PRIOR FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
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             AATCACTTTGCATTTTCCGAGAAAATCCTCATCATTTCAGGGCGGTGGTGGAGAACTACA
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APPLICANT: Hedden, Peter
APPLICANT: Phillips, Andrew L
APPLICANT: Phillips, Andrew L
APPLICANT: Phillips, Andrew L
TILE OF INVENTION: Gibberellin 2-Oxidase
FILE REFERENCE: 0623.0970000
CURRENT APPLICATION NUMBER: US/09/719,108
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: GE 9812821.8
PRIOR FILING DATE: 1999-06-11
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTING DATE: 1998-07-15
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; Sequence 5, Application US/09719108
; Patent No. 6670527
; GENERAL INFORMATION:
; APPLICANT: Thomas, Stephen G
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NAME/KEY: misc feature
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Query Match 35.8%; Score 356.6; DB 3; Best Local Similarity 63.2%; Pred. No. 2.8e-109; Matches 586; Conservative 0; Mismatches 329;
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1023 ACAAGGAGTTCACATGGGATGAGTACAAGAAGGCTGCCTACAAATCAAGGCTTGGAGACA 1082
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     TAAGGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGATTCGTGCTTCA
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Lee, Jian Ming
Sakai, Hajime
Weng, Zude
Caimi, Perry G
Anderson, Shawn
RENERTION: Plant Metabolism Genes
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CURRENT APPLICATION NUMBER: US/09/614,912

CURRENT FILING DATE: 2000-07-12

PRIOR FILING DATE: 1999-07-12

PRIOR FILING DATE: 1999-07-12

PRIOR FILING DATE: 1999-07-12

PRIOR PILING DATE: 1999-07-12

PRIOR PILING DATE: 1999-07-12

PRIOR PILING DATE: 1999-12-15

PRIOR PILING DATE: 1999-12-11

NUMBER OF SEQ ID NOS: 204

SOFTWARE: Microsoft Office 97

LENGTH: 1555
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Patent No. 6677502
GENERAL INFORMATION:
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Rafalski, Antoni
Orozco, Buddy
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FILE REFERENCE: BB1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            492 CCTGCACCGTCCCGTCCTGCG------CGGTCTTCCGGGCCGCTCTGAACGAGTACA 542
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee, Jian Ming
Sakai, Hajime
Weng, Zude
Calmi, Perry G
Anderson, Shawn
INVENTION: Plant Metabolism Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: UNA (1976) CURRENT FILING DATE: 2000-07-12 PRIOR APPLICATION NUMBER: 60/143,401 PRIOR FILING DATE: 1999-07-12 PRIOR FILING DATE: 1999-07-12 PRIOR PILING DATE: 1999-07-12 PRIOR APPLICATION NUMBER: 60/146,650 PRIOR APPLICATION NUMBER: 60/146,650 PRIOR PILING DATE: 1999-07-30 PRIOR FILING DATE: 1999-07-30 PRIOR PILING DATE: 1999-12-15 PRIOR APPLICATION NUMBER: 60/170,966 PRIOR APPLICATION NUMBER: 60/170,966 PRIOR PILING DATE: 1999-12-15 PRIOR APPLICATION NUMBER: 60/172,946 PRIOR PILING DATE: 1999-12-21 PRIOR PILING DATE: 2004-2016 PRIOR PRIOR PILING DATE: 2004-2016 PRIOR PILING DATE: 2004-2016 PRIOR PRIOR PILING DATE: 2004-2016 PRIOR PILING DATE: 2004-2016 PRIOR PRIOR PILING DATE: 2004-2016 PRIOR PILING DATE: 2004-2016 PRIOR PRIOR PILING DATE: 2004-2016 PRIOR PILING DATE: 2004-2016 PRIOR PRIOR PILING DATE: 2004-2016 PRIOR PILING DATE: 2004-2016 PRIOR PRIOR PILING DATE: 2004-2016 PRIOR PILING DATE: 2004-2016 PRIOR PRIOR PILING DATE: 2004-2016 PRIOR PILING DATE: 2004-2016 PRIOR PRIOR PILING DATE: 2004-2016 PRI
Sequence 3, Application US/09614912
Patent No. 6677502
                                                                                                                                                                      Allen, Steve
Rafalski, Antoni
Orozco, Buddy
Miao, Gou-Hau
Famodu, Omolayo O.
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ORGANISM: Oryza sativa
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FILE REFERENCE: BB1
                                                                                                                  GENERAL INFORMATION:
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793 GCTGACACAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACCAGCGTTGAGTGAA 852
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                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Brown, Sherri M.
APPLICANT: Heck, Gregory R.
APPLICANT: Filler, Kenneth J.
APPLICANT: Filler, Red D.
APPLICANT: Logusch, Eugene W.
APPLICANT: Logusch, Eugene W.
APPLICANT: Logusch, Eugene W.
APPLICANT: Ream, Joel E.
APPLICANT: Ream, Joel E.
APPLICANT: Ream, Joel E.
APPLICANT: Represelve Sherry J.
APPLICANT: Repure Methods for controlling gibberellin levels
FILE REFERENCE: MOBT:216
CURRENT APPLICATION NUMBER: US/09/371,307A
CURRENT FILING DINOS: 899-08-10
NUMBER OF SEQ ID NOS: 899-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
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Pred. No. 5.8e-93;
0; Mismatches 167; Indels
                                                                                                                                                                Sequence 67, Application US/09371307A
Patent No. 6723897
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1087 CAGTTTGAGAA 1097
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Matches 436; Conservative
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; LOCATION: (726)
; OTHER INFORMATION: n
US-09-371-307-67
                                                                                                          RESULT 12
US-09-371-307-67
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LENGTH: 783
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Best Local Similarity 59.3
Matches 576; Conservative
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; TYPE: DNA; CORGANISM: Zea mays US-09-614-912-1
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APPLICANT: Brown, Sherri M.
APPLICANT: Piller, Kenneth J.
APPLICANT: Piller, Kenneth J.
APPLICANT: Elich, Tedd D.
APPLICANT: Elich, Tedd D.
APPLICANT: Rao, Sudabathula
APPLICANT: Logusch, Sherry J.
TITLE OF INVENTION: Methods for controlling gibberellin levels
TILE OF INVENTION: Methods for controlling gibberellin levels
TILE REFERENCE: MOST: 1999-08-10
CURRENT FILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 66
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Patent No. 6723897
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US-09-371-307-66
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Best Local Similarity 63.2
Matches 261; Conservative
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ORGANISM: Glycine
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US-09-371-307-68
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Sequence 71, Application US/09371307A

Patent No. 6723897

GENERAL INFORMATION:

APPLICANT: Brown, Sherri M.

APPLICANT: Piller, Kenneth J.

APPLICANT: Kiehor, Ganesh M.

APPLICANT: Rao, Sudabathula

APPLICANT: Logusch, Eugene W.

APPLICANT: Logusch, Sherry J.

APPLICANT: Logusch, Sherry J.

TITE OF INVENTYON: Methods for controlling gibberellin levels

FILE REFERENCE: MOST.126

CURRENT FILING DATE: 1999-08-10

NUMBER OF SEQ ID NOS: 89

SOFTWARE: Patentin Ver. 2.0

SEDID NO. 11
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                                              APPLICANT: Brown, Sherri M.
APPLICANT: Heck, Gregory R.
APPLICANT: Piller, Kenneth J.
APPLICANT: Piller, Kenneth J.
APPLICANT: Elich, Tedd D.
APPLICANT: Elich, Tedd D.
APPLICANT: Ream. Joel E.
APPLICANT: Ream. Joel E.
APPLICANT: Ream. Joel E.
APPLICANT: Ream. Joel E.
APPLICANT: MONST:216
TILE REFERENCE: MONST:216
CURRENT FILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 89
SOFTHARE: PatentIn Ver. 2.0
SEQ ID NO 68
LENGTH: 406
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Best Local Similarity 66.6%; Pred. No. 1.7e-41;
Matches 279; Conservative 0; Mismatches 113; Indels 27
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Sequence 68, Application US/09371307A
Patent No. 6723897
GENERAL INFORMATION:
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NAME/KEY: unsure
LOCATION: (306)
OTHER INFORMATION: n = a, c,
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Sequence 67, Appl
Sequence 6183, Ap
Sequence 111, Appl
Sequence 123307,
Sequence 7861, Ap
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                                                                     December 27, 2005, 17:51:22 ; Search time 936.171 Seconds (without alignments) 8797.858 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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| /cgn2_6/prodata/1/phbpna/USSO8_PUBCOMB.seq:*
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                                    100.0%; Score 996; D
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 ; LENGTH: 1318
TYPE: DNA
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LENGTH: 1318
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| Publication No. US20040229357A1
| GENERAL INFORMATION:
| APPLICANT: Thomas, Stephen G
| APPLICANT: Thomas, Stephen G
| APPLICANT: Hedden, Peter
| APPLICANT: Phillips, Andrew L
| TILLE OF INVENTION: Gibberellin 2-Oxidase
| FILE REFERENCE: 0623.0970000
| CURRENT APPLICATION NUMBER: US/10/670,454
| CURRENT APPLICATION NUMBER: US/09/719,108
| PRIOR APPLICATION NUMBER: PCT/GB99/01857
| PRIOR FILING DATE: 2000-12-08
| PRIOR FILING DATE: 1999-06-11
| PRIOR PLING DATE: 1999-06-12
| PRIOR PLING DATE: 1998-06-12
| PRIOR FILING DATE: 1998-06-12
| PRIOR FILING DATE: 1998-07-15
| NUMBER: OSEQ ID NOS: 16
| SEQ ID NO 1
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; Sequence 62, Application US/10401321
; Publication No. US200302336/9A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Kilshore, Ganesh M.
; APPLICANT: Blich, Tedd D.
; APPLICANT: Bouseh, Busene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Room, Joel E.
; APPLICANT: Logusch, Sherry J.
; APPLICANT: Baerson, Scott R.
; TITLE OF INVENTION: Methods for Controlling Gibberellin Levels
; TILE REFERENCE: 11899.0216. DVUSQ1 (MOBT: 216-1)
; CURRENT APPLICATION NUMBER: US/10/401,321
; CURRENT APPLICATION NUMBER: US/10/401,321
; CURRENT PAPLICATION NUMBER: OF SEQ ID NOS: 89
; SOFTWARE: Patentin version 3.2
; SEQ ID NO S: 89
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APPLICANT: Brown, Sherri M.
APPLICANT: Heck, Gregory R.
APPLICANT: Piller, Kenneth J.
APPLICANT: Kishor, Ganesh M.
APPLICANT: Logusch, Eugene W.
APPLICANT: Logusch, Eugene W.
APPLICANT: Logusch, Sherry J.
TILE OF INVENTION: Methode for controlling gibberellin levels
FILE REFERENCE: MOBT:216
CURRENT APPLICANTON VUMBER: US/09/371,307A
CURRENT FILING DATE: 1999-08-10
CURRENT FILING DATE: 1999-08-10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 62
LENGTH: 1359
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Pred. No. 1.7e-270;
1; Mismatches 97;
 961 AATAGGCTTGCCCCTTTCCAGAAATCTGCTGCTGAT
                                                                                                                     Sequence 62, Application US/09371307A Patent No. US20020053095A1 GENERAL INFORMATION:
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CORGANISM: Glycine max
US-09-371-307-62
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Best Local Similarity
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                                                                                                                                                                                                                                                                                              Score 424.4; DB 3;
Pred. No. 4.7e-133;
0; Mismatches 291;
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; LENGTH: 1026
                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1350
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Best Local Similarity 67.5%;
Matches 612; Conservative
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Patent No. US20020160378A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Harper, Jeff

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

TITLE OF INVENTION: SAME, AND METHODS OF USE

FILLE REFRERENCE: SCR.P1300-3

FILLE REFRERENCE: SCR.P1300-3

FILLE REPRERENCE: 2001-08-24

CURRENT APPLICATION NUMBER: US 60/227,866
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     571 GC---GGCGGAGGAAGAGGCGGAGAAGATGGTGAAGGTGGGGTTTGGGGAACACACAGAC
                                                                                              ACAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACCAGCGTTGAGTGAAATATA
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Pred. No. 5.3e-133;
0; Mismatches 291; Indels
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Publication No US20040229357A1
GENERAL INFORMATION:
APPLICANT: Thomas, Stephen G
APPLICANT: Phillips, Andrew L
TITLE OF INVENTION: Gibberellin 2-Oxidase
FILE REFERENCE: 0623.0970000
CURRENT APPLICATION NUMBER: US/10/670,454
CURRENT APPLICATION NUMBER: US/09/719,108
FILE REPERIOR DATE: 2003-09-26
FRIOR FILING DATE: 1999-06-11
FRIOR FILING DATE: 1999-06-11
FRIOR APPLICATION NUMBER: GB 9812821.8
FRIOR FILING DATE: 1998-06-12
FRIOR FILING DATE: 1998-07-15
NUMBER: OF SEQ ID NOS: 16
SEQ ID NO 7
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Best Local Similarity 67.5
Matches 612; Conservative
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| Sequence 1350, Application US/09938842A
| Publication No. US20040009476A9
| GENERAL INFORMATION:
| APPLICANT: Harper, Joeff
| APPLICANT: Kreps, Joel |
| APPLICANT: Wang, Xun |
| APPLICANT: Wang, Xun |
| APPLICANT: Wang, Xun |
| APPLICANT: Ress. SAME, AND METHODS OF USE |
| TITLE OF INVENTION: SAME, AND METHODS OF USE |
| TITLE OF INVENTION: SAME, AND METHODS OF USE |
| FILE REFERENCE: SCRIP1300-3 |
| CURRENT FILING DATE: 2001-08-24 |
| PRIOR APPLICATION NUMBER: US 60/227, 866 |
| PRIOR FILING DATE: 2001-01-16 |
| PRIOR FILING DATE: 2001-01-16 |
| PRIOR PELICATION NUMBER: US 60/300,111 |
| PRIOR APPLICATION NUMBER: US 60/300,111 |
| PRIOR APPLICATION NUMBER: US 60/300,111 |
| PRIOR SEQ ID NOS: 5379 |
| LENGTH: 1026 |
| LENGTH: LENGT
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                                                                                     979 CAGAAA 984
                                                                                                                                         988 GAGAAA 993
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US-09-938-842A-1350
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Best Local S:
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                                                                                                                                                                                        Length 1403;
                                                                                                                                                                                        Score 418.2; DB 3;
Pred. No. 7.4e-131;
0; Mismatches 318;
                                                                                                                                                                                           42.0%;
                   SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 64
LENGTH: 1403
                                                                                                                                                                                      Query Match
Best Local Similarity 66.2
Matches 657; Conservative
  83
  NUMBER OF SEQ ID NOS:
                                                                                           ; TYPE: DNA
; ORGANISM: Glycine
US-09-371-307-64
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                                                                              GTGTCGTACAAGGTGTTGGAAGAAGAACTAGGGATAGAGCCAAGGGCACACT
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US-09-371-307-64
i Sequence 64, Application US/09371307A
j Patent No. US20020053095A1
j GENERAL INFORMATION;
APPLICANT Brown, Sherri M.
APPLICANT Heck, Gregory R.
APPLICANT Kishore, Ganesh M.
APPLICANT Educk, Eugene W.
APPLICANT: Ream, Joel E.
APPLICANT: Ream, Joel E.
APPLICANT: Ream, Joel E.
APPLICANT: Ream, Joel E.
APPLICANT: Ream, Sudabathula
FILE OF INVENTION: Methods for controlling gibberellin levels
FILE REFERENCE: MOSF:216
GURRENT APPLICATION NUMBER: US/09/371,307A
; CURRENT FILING DATE: 1999-08-10
                                                 CCCGACCCTTTCGGCTATGGTAGCAAGAGGATTGGCCCAAACGGTGATGTCGGTT
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Sequence 21951, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILIS REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT3847_119826C.1
US-10-424-599-21951
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APPLICANT: Brown, Sherri M.
APPLICANT: Piller, Kenneth J.
APPLICANT: Piller, Kenneth J.
APPLICANT: Filshore, Gamesh M.
APPLICANT: Elich, Tedd D.
APPLICANT: Loquesch, Eugene W.
APPLICANT: Loquesch, Eugene W.
APPLICANT: Ream, Joel E.
APPLICANT: Ream, Joel E.
APPLICANT: Applicant: Loquesch, Sherry J.
APPLICANT: Baerson, Scott R.
TITLE OF INVENTION: Methods for Controlling Gibberellin Levels
FILE REPRENCE: 11899.0216.DVUSO1 (MOBT:216--1)
CURRENT APPLICANT: 2003-03-27
NUMBER OF SEQ ID NOS: 89
SOUTHARE: PatentIn Version 3.2
SEQ ID NO 64
LENGTH: 1403
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                                                                                                                                                     AATAGGCTTGGACATTTTGAGAGAATTGTTGCT 1123
                                                                                             AATAGGCTTGCCCCTTTCCAGAAATCTGCTGCT 993
                                                                                                                                                                                                                                                                                                    Sequence 64, Application US/10401321
Publication No. US20030233679A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 66.2
Matches 657; Conservative
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; ORGANISM: Glycine max
US-10-401-321-64
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                   PRIOR APPLICATION NUMBER: GB 9812821.8
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: GB 9815404.0
PRIOR PILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 16
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Publication No. US20040229357A1
GENERAL INFORMATION:
APPLICANT: Homas, Stephen G
APPLICANT: Hedden, Peter
TITLE REPERENCE: 0623.0970000
CURRENT APPLICATION NUMBER: US/10/670,454
CURRENT FILING DATE: 2003-09-26
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: US/09/719,108
PRIOR APPLICATION NUMBER: US/09/719,108
PRIOR APPLICATION NUMBER: PCT/GB99/01857
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GENERAL INFORMATION:

APPLICANT: Kayano, Toshiaki

APPLICANT: Kayano, Toshiaki

APPLICANT: Mateuoka, Makoto

APPLICANT: Saito, Tamio

APPLICANT: Saito, Tamio

APPLICANT: Sakanoto, Tomoaki

APPLICANTON: Tomoaki

APPLICANT: Sakanoto, Tomoaki

APPLI
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60.9%; Pred. No. 4.8e-109;
ive 0; Mismatches 375; IndelB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 35.5
Best Local Similarity 60.9
Matches 598; Conservative
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OTHER INFORMATION:
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| Publication No. US20040229357A1
| GENERAL INFORMATION |
| APPLICANT: Thomas, Stephen G |
| APPLICANT: Thomas, Stephen G |
| APPLICANT: Hedden, Peter |
| APPLICANT: Phillips, Andrew L |
| TITLE OF INVENTION: Gibberellin 2-Oxidase |
| FILE REFERENCE: 0623.0970000 |
| CURRENT FILING DATE: 2003-09-26 |
| CURRENT FILING DATE: 2000-12-08 |
| PRIOR PILING DATE: 1999-06-11 |
| PRIOR PILING DATE: 1999-06-11 |
| PRIOR FILING DATE: 1999-06-12 |
| PRIOR PILING DATE: 1999-06-12 |
| PRIOR FILING DATE: 1998-06-15 |
| PRIOR FILING DATE: 1998-06-15 |
| NUMBER OF SEQ ID NOS: 16 |
| SOFTWARE: PatentIn Ver: 2.1
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NAME/KEY: misc feature
LOCATION: (1243, 1265)
OTHER INFORMATION: unidentified residue
US-10-670-454-5
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ORGANISM: Arabidopsis thaliana
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LENGTH: 1318
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 78659
LENGTH: 1260
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35.5%; Score 354; DB 7; Length 12
Best Local Similarity 60.9%; Pred. No. 5.6e-109;
Matches 598; Conservative 0; Mismatches 375; Indels
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ORGANISM: Oryza sativa
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Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Lou, Yihua
APPLICANT: ANOUNG K.
APPLICANT: ANOUNG K.
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Blants
TITLE OF INVENTION: Plants
FILE OF INVENTION: Plants
FILE REPERENCE: 38-21 (5322) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
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LENGTH: 1611
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Pred. No. 2.5e-95;
0; Mismatches 383; Indels 12;
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US-10-425-115-69575
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Best Local Similarity 59.3%;
Matches 576; Conservative
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                                                                              December 27, 2005, 18:17:41 ; Search time 179.487 Seconds (without alignments) 2879.764 Million cell updates/sec
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    /cgn2_6/ptodata/2/pubpna/USO1_NEW_PUB.seq:*
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version 5.1.6
- 2005 Compugen Ltd.
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US-11-152-892-3
US-11-12-998-45
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US-11-112-908-45
US-11-17-187-209
US-11-17-187-209
US-11-112-908-140
US-11-112-908-140
US-11-117-187-212
US-10-750-185-56890
US-11-17-187-199
US-10-995-561-1325
US-10-995-561-1325
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                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                      - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
GenCore (c) 1993
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254 ATATCAATGGATGTTGGAGAAGATGAGACAAGAGCAAATTAGGGTCTTTAGAGAGCCT 313
194 AAGGAAGCGATTGCGAGAGCTTCGAGGGAGTGGGGGATTTTTTCAAGTGATAAACCATGGA 253
                                                     172 GITCCATTGGAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCT
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4.0%; Score 40; DB 7; Length 1011;
Best Local Similarity 53.1%; Pred. No. 0.0025;
Matches 85; Conservative 0; Mismatches 75; Indels
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                                                          Sequence 3, Application US/11152892

Sequence 3, Application US/11152892

Publication No. US20050251883A1

GENERAL INFORMATION:

APPLICANT: Amasino, Richard M.

APPLICANT: Amasino, Richard M.

APPLICANT: Michaels, Scott D.

APPLICANT: Michaels, Scott D.

TITLE OF INVENTION: Dwarfism Genes and Dwarf Plants

FILE REFERENCE: 960296.97665

CURRENT APPLICATION NUMBER: US/11/152,892

CURRENT APPLICATION NUMBER: US/11/152,892

CURRENT APPLICATION NUMBER: US/10/155,435

PRIOR FILING DATE: 2002-05-23

NUMBER OF SEQ ID NOS: 12

SEQ ID NO 3

LENGTH: 1011

TWENT: 1011
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Publication No. US20050251883A1
GENERAL INFORMATION:
APPLICANT: Amesino, Richard M.
APPLICANT: Schomburg, Fritz M.
APPLICANT: Bizall, Colleen M.
TITLE OF INVENTION: Dwarfism Genes and Dwarf Plants
FILE REPERENCE: 960296.97605
CURRENT FILING DATE: 2005-06-15
FRICK APPLICATION NUMBER: US/11/152,892
CURRENT FILING DATE: 2005-06-15
FRICK APPLICATION NUMBER: US/10/155,435
FRICK RELING DATE: 2005-06-15
FRICK REPERENCE: SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
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ORGANISM: Arabidopsis
US-11-152-892-2
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LENGTH: 3861
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2392 ACAAAAATAAAGCAAAGAGTGTTAGTTGATACAAAATAATCAACATTTTACAGTATGGAT 2333
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Pred. No. 0.21;
0; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Harris, Cole
APPLICANT: Harris, Cole
APPLICANT: Harris, Cole
APPLICANT: Harris, Cole
TILE OF INVENTION: Breast Cancer Biomarkers
FILE OF INVENTION: 04.64-US
CURRENT FILING DATE: 2005-04-22
PRIOR APPLICATION NUMBER: US 60/564,758
PRIOR FILING DATE: 2004-06-01
PRIOR PILING DATE: 2004-01-01
PRIOR PILING DATE: 2004-01-01
PRIOR APPLICATION NUMBER: US 60/631,702
PRIOR APPLICATION NUMBER: US 60/631,826
PRIOR APPLICATION NUMBER: US 60/631,826
PRIOR FILING DATE: 2004-11-07
NUMBER OF SEQ ID NOS: 511
SOFTWARE: Patentin version 3.3
SEQ ID NO 44
TURNET NANAE: NANAER: N
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APPLICANT: Harris, Cole
APPLICANT: Davis, Lisa M.
TITLE OF INVENTION: Breast Cancer Biomarkers
FILE REFERENCE: 04-164-US
CURRENT PILING DATE: 2005-04-22
PRIOR APPLICATION NUMBER: US 60/564,758
PRIOR APPLICATION NUMBER: US 60/575,978
PRIOR PILING DATE: 2004-04-23
PRIOR APPLICATION NUMBER: US 60/575,978
PRIOR PILING DATE: 2004-06-01
PRIOR PILING DATE: 2004-10-07
PRIOR PILING DATE: 2004-11-30
PRIOR PILING DATE: 2004-11-30
PRIOR APPLICATION NUMBER: US 60/633,826
PRIOR FILING DATE: 2004-11-30
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Publication No. US20050260659A1
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Best Local Similarity 58.8%;
Matches 67; Conservative (
232 CAGTCCGAGAAA 243
                                                                                                    314 TTTGACAAGAAA 325
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; ORGANISM: Homo sapiens
US-11-112-908-44
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US-11-117-187-209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 GICCGAGAAAGACAGAGCIGGICCCCCCGACCCTITCGGCTAIGGIAGCAAGAGGATIGG 293
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                                                                                                 Query Match 3.9%; Score 38.8; DB 7; Length 182314; Best Local Similarity 58.8%; Pred. No. 0.24; Matches 67; Conservative 0; Mismatches 47; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 3.6%; Score 36; DB 7; Length 2171; Best Local Similarity 49.5%; Pred. No. 0.11; Matches 93; Conservative 0; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Schomburg, Fritz M.
APPLICANT: Schomburg, Fritz M.
APPLICANT: Michaels, Scott D.
APPLICANT: Michaels, Scott D.
TITLE OF INVENTION: Dwarfism Genes and Dwarf Plants
FILE REFERENCE: 960296.97605
CURRENT APPLICATION NUMBER: US/11/152,892
CURRENT FILING DATE: 2005-06-15
PRIOR FILING DATE: 2005-06-23
PRIOR FILING DATE: 2002-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19, Application US/11174166
Publication No. US20050260669A1
GENERAL INPORMATION:
APPLICANT: Kirsch, Wolff M.
APPLICANT: Lennart, Anton
APPLICANT: Kelln, Wayne J.
APPLICANT: Kelln, Kayne J.
APPLICANT: Levine, RederKyung
APPLICANT: Levine, Rodney L.
APPLICANT: Rouault, Tracey
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/11152892
Publication No. US20050251883A1
GENERAL INFORMATION:
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SEQ ID NO 1
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                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-45
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; ORGANISM: Arabidopsis
US-11-152-892-1
LENGTH: 182314
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Sequence 209, Application US/11117187

Sequence 209, Application No. US2005026560A1

Sequence 209, Application No. US2005026560A1

GENERAL INFORMATION:

APPLICANT: PREUSS, DAPHNE

TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS

FILE REFERENCE: ARCD: 309US

CURRENT FILING DATE: 2006-04-28

PRIOR APPLICATION NUMBER: US/10/117,187

CURRENT FILING DATE: 2000-03-17

PRIOR FILING DATE: 1999-03-18

PRIOR FILING DATE: 1999-03-18

NUMBER OF SEQ ID NOS: 212

SEQ ID NO 209

LEMCHANE: PATCH OF THE TOWN NUMBER: US/10/120

SEQ ID NO 209

LEMCHANE: PATCH OF THE TOWN NUMBER: US/10/120

SEQ ID NO 209

LEMCHANE: PATCH OF THE TOWN NUMBER: US/10/120

SEQ ID NO 209
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TITLE OF INVENTION: IRON REGULATING PROTEIN-2 (IRP-2) AS FITLE OF INVENTION: A DIAGNOSTIC FOR NEURODEGENERATIVE DISEASE FILE REFERENCE: LOMAU.140C US/11/174,166
CURRENT APPLICATION NUMBER: US/11/174,166
CURRENT FILING DATE: 2005-07-01
PRIOR PAPLICATION NUMBER: 60/222,863
PRIOR PAPLICATION NUMBER: 60/222,863
PRIOR FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 20
SOFTWARE: RateSEQ for Windows Version 4.0
SEQ ID NO 19
LENGTH: 3770
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Pred. No. 0.35;
0; Mismatches
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; Publication No. US20050260659A1
; GENERAL INFORMATION:
APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
FILE REPERENCE: 04-164-05
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US-11-117-187-209
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Matches 62; Conservative
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                                                       501 AAGCAGGTTGCTGAAGGATGAGAAAGTGATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              381 AGAAAATCCTCATCATTTCAGGGGGGGGGGGGGAAACTACATTACAGCAGTGAAGAACAT
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Pred. No. 26;
0; Mismatches 75; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.3%; Score 33; DB 7; Length 921; Best Local Similarity 51.0%; Pred. No. 0.66; Matches 78; Conservative 0; Mismatches 75; Indels
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Publication No. US20050260659A1
GENERAL INPORMATION:
APPLICANT: Harris, Cole
APPLICANT: Davis, Lisa M.
TITLE OF INVENTON: Breast Cancer Biomarkers
FILE REFREENCE: 04-164-US
CURRENT APPLICATION NUMBER: US/11/112,908
CURRENT APPLICATION NUMBER: US 60/564,758
FRIOR APPLICATION NUMBER: US 60/559,978
PRIOR APPLICATION NUMBER: US 60/575,978
PRIOR APPLICATION NUMBER: US 60/51,702
PRIOR FILING DATE: 2004-06-01
PRIOR FILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-12-07
NUMBER OF SEQ ID NOS: 511
SOFTWARE: Patentin version 3.3
SEQ ID NO 40
LENGTH: 180862
CURRENT APPLICATION NUMBER: US/11/112,908
CURRENT FILING DATE: 2005-04-22
PRIOR PRILOR TILING DATE: 2006-04-23
PRIOR FILING DATE: 2004-06-01
PRIOR PLING DATE: 2004-06-01
PRIOR PLING DATE: 2004-06-01
PRIOR PLING DATE: 2004-11-30
PRIOR PLING DATE: 2004-11-30
PRIOR PILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-11-30
SOFTWARE: PARIOR PRIOR PR
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Best Local Similarity 51.0°
Matches 78, Conservative
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ORGANISM: Homo sapiens
US-11-112-908-40
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; ORGANISM: Homo sapiens
US-11-112-908-140
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US-11-112-908-40/c
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104835 TAÀAAAAGGAAAAGACTAGTTTTTTTTTATTACAACAACTCACAAACACCAATGATCT 104894
Sequence 212 Application US/11117187

Sequence 212 Application US/11117187

Sequence 212 Application US/11117187

Sequence 212 Application US. US2005026560A1

GENERAL INFORMATION:

APPLICANT: PREUSS, DAPHNE

APPLICANT: COPENHAVER, GREGORY

TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS

FILE REFERENCE: ARCD:309US

CURRENT APPLICATION NUMBER: US/11/117,187

CURRENT APPLICATION NUMBER: US/09/531,120

PRIOR APPLICATION NUMBER: 60/125,219

PRIOR FILING DATE: 1999-03-18

SOFTWARE: PACENTIN VOIC: 2.1

SEQ ID NOS: 212

LENGTH: 163317
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APPLICANT: MAI GENOMICS, INC.
APPLICANT: ERRR, Richard
APPLICANT: ERRR, Richard
APPLICANT: ROSENEELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TILLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MAILO-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 6; Length 1138;
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Publication No. US20050260603A1
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US-10-750-185-56890
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SOFTWARE: Patentin version 3.1
SEQ ID NO 56890
LENGTH: 1138
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Best Local Similarity 57.4<sup>§</sup>
Matches 58; Conservative
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546
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                                                                                                     283 CTGACATTTTAGCTGAGGCTGAAGATGGAGAATGAGCCAGTTATTTAATGTGCTGGGGA 224
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Fublication No. US2005026656A1

GENERAL INFORMATION:
APPLICANT: PREUSS, DAPHNE
APPLICANT: COPENHAPER, GREGORY
TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
FILE REPEREBRUCE: ARCD:309US
CURRENT APPLICATION NUMBER: US/11/117,187
CURRENT PILING DATE: 2005-04-28
FRIOR FILING DATE: 2006-03-17
PRIOR FILING DATE: 2006-03-18
FRIOR FILING DATE: 199-03-18
FRIOR FILING DATE: 199-03-18
                                                              CAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGATTCGTGCTTCAGGTTG
                                                                                                                                             142 TTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCCATTGGAGTTAATGGCCAATTTAGAA
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Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, KIRSTEN V.
TITUE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 091386.6000-00000.
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
FRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PATENTIN VETSION 3.3
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3.2%; Score 31.6; DB 7; Length 10:
Best Local Similarity 55.5%; Pred. No. 53;
Matches 61; Conservative 0; Mismatches 49; Indels
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SOFTWARE: PatentIn Ver. 2.1
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; ORGANISM: Homo sapiens
US-11-121-086-44
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LENGTH: 101786
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US-11-121-086-44
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presture:
    NAME/KEY: misc feature
    LOCATION: (1)...(187786)
    CTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-:
US-10-995-561-13474
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APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLOOISS9
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: PRESENCE OF WINDOWS Version 4.0
SEQ ID NO 13474
LENGTH: 187786
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                                                                                                                                                                                                                                                        474 GTTGGGGATAAGGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGATTC
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      DB 7; Length 167116;
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                                                                                                                        56; Indels
3.2%; Score 31.4; Di
Similarity 53.7%; Pred. No. 87;
55; Conservative 0; Mismatches
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Publication No. US20050272054A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 54.9
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ORGANISM: Homo sapiens
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US-10-995-561-13474/c
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Query Match
Best Local S
Matches 65
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Title: Perfect score:

Sequence:

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Searched:

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AX302041 Cucurbita AK506655 Sequence BT004464 Arabidops AJ132436 Arabidops BD243013 Enzyme. 7 AR444995 Sequence AR008677 Sequence BT002987 Arabidops AR125213 Vigna ang AR452817 Sequence AR50821 Sequence AR508410 Sequence AR508410 Sequence AR50835 Pisum sat AR56935 Pisum sat AR101382 Pisum sat AK600714 Oryza sat AK60714 Oryza sat AK60666 Oryza sat AK609350 Oryza sat AR609150 Oryza sat AR009120 Inctum SAK09310 Inctum SAK09310 Inctum SAK09310 Inctum SAK95815 Sequence
AX008671 Sequence
A132438 Phaseolus
AB181372 Vigna ang
AB528429 Sequence
AX59429 Nerium ol
AB125232 Nicotiana
AY588978 Nerium ol
Y09113 Minacrocarp
A315663 Cucurbita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAT 08-NOV-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gilbertson, L., Krieger, E., Zhang, W. and Ye, X.
Dna constructs and methods to enhance the production of
commercially viable transgenic plants
Patent: WO 2004092390-A 3 28-OCT-2004;
Monsanto Technology LLC (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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/mol_type="unassigned DNA"
/db_xref="taxon:3886"
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AR452821
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ATH132436
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AR452818
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AB031207
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Location/Qualifiers
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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CQ899251
LOCUS
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-MODEL=france+ p2n. model -DEV=xlh
-MODEL=france+ p2n. model -DEV=xlh
-MODEL=france- p2099/app_query.fasta_1.519
-Q=/cgn2_1/USPTO_spool/US10670454/runat_27122005_124840_29099/app_query.fasta_1.519
-DB=GenEmb1 -QFWT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bite -STRAT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UNFRYT=ptc -NORM=ext -HEAPSIZE=500 -MINLENN=0 -MAXLENS=2000000000
-USRE-US10670454 @CGN 1 1 4939 @runat_27122005_124840_29999 -NCPU=6 -ICPU=3
-NO MANAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPEDCCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=0 -TRREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CQ899251 Sequence
BD243009 Enzyme. 7
AR444991 Sequence
                                                                                                                                                                                                      December 28, 2005, 00:38:54; Search time 6072 Seconds (without alignments) 3098.680 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                     1 MVVLSQPALNQFFLLKPFKS...........AAYTSRLADNRLAPFQKSAA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                   GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                            using frame plus p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5883141 segs, 28421725653 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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BD243009
AR444991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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coccineus (scarlet runner
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
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Phaseolus.
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Patent: JP 2002518005-A 1 25-JUN-2002;
THE UNIVERSITY OF BRISTOL
OS Phaseolus coccineus (scarlet runner bean)
PN JP 2002518005-A/1
PD 25-JUN-2002
PP 11-JUN-1999 JP 2000554838
PP 11-JUN-1999 GB 9812821.8,15-JUL-1998 GB 9815404.0 PI
STEPHEN GREGORY THOMAS, PETER HEDDEN, ANDREW LEONARD PHILLIPS PC
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Thomas, S.G., Hedden, P. and Phillips, A.L.
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            961 AATAGGCTTGCCCCTTTCCAGAAATCTGCTGCT
  321 AsnArgLeuAlaProPheGlnLysSerAlaAla
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PC C12N5/00,C12N5/00,C12N15/00
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1 (bases 1 to 1318)

Thomas, S.G., Hedden, P. and Phillips, A.L. Gibberellin 2-oxidase
Patent: US 6670527-A 1 30-DEC-2003;
The University of Bristol; Bristol;
GBX;
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Sequence 1 from patent US 6670527.
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PCO132438
Phaseolus coccineus mRNA for GA 2-oxidase, gene ga2ox1.
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AJ132438.1 GI:4678585
Phaseolus coccineus
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Submitted (18-JAN-1999) Phillips A.L., Plant Sciences, IACR Long
Ashton Research Station, Long Ashton Research Station, Bristol,
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/product="GA_2-oxidase"
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PHILLIPS ANDREW LEDONARD (GB); HEDDEN PETER (GB); UNIV BRISTOL (GB);
THOWAS STEPHEN GREGORY (GB)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyaspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro 120
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                                                                                                                                                      Phaseolus coccineus
bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosida, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
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                                                                       linear
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Matches:
Conservative:
Mismatches:
Indels:
 1. .1318
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                                                                                                                                                                                                                                      Phillips, A.L., Hedden, P. and Thomas, S.G.
                                                                        ONA
                                                                    AX008671 1318 bp
Sequence 1 from Patent WO9966029.
AX008671
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/product="gibberellin 2-oxidase"
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/db xref="G1:67077812"
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                                                                                                                                                                                                                                                                                                                  AB181372 1360 bp mRNA linear PLN 09-JUN-2005 Vigna angularis VaGA20xAl mRNA for gibberellin 2-oxidase, complete cds.
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Nakajima, M., Xu,Z., Park,S., Tomioka,K., Sakane,M. and Yamaguchi,I.

Direct Submission

Direct Submission

Submitted (08-JUN-2004) Masatoshi Nakajima, The University of

Tokyo, Dept. Appl. Biol. Chem., Fac. of Agriculture; 1-1-1 Yayoi,

Bunkyo, Tokyo, 113-8657, Japan

Fax:81-3-5841-8025)

Location/Qualifiers

1. 1360

/organism="Wigna angularis"
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Unpublished
                                                                                   300
                                                                                                                 967
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Vigna angularis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Vigna.
                   280
                                                907
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                                                                                   AlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCysLeu
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                                                  848 caradegriringecreaceaecaaceaecraacerrarcaarearcraciringeaecea
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Pred. No.:
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AB181372
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        ArgleuanhistyrProprocysProGluValGlnAlaLeuanhistyanheuvalGly

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08-OCT-2004

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Logusch, E.W., Baerson, S.R.

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121 LysSerLeuCysIlePheArgGluAsnProHisHisPheArgAlaValValGluAsnTyr 140
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                                                                                                     1 (bases 1 to 1359)
Brown,S.M., Elich,T.D., Heck,G.R., Kishore,G.M.,
Logusch,S.J., Piller,K.J., Rao,S., Ream,J.E. and
Methods for controlling gibberellin levels
Patent: US 6723897-A 62 20-APR-2004;
Monsanto Technology, LLC; St. Louis, MO
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
                                     6723897
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AR528429
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        ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly

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/brotein id="AAT92094.1"
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1 (bases 1 to 1245)
Ubeda-Tomas, S., Garcia-Martinez, J.L. and Lopez-Diaz, I.
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Ubeda-Tomas, S., Garcia-Martinez, J.L. and Lopez-Diaz, I.
Direct Submission
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Nerium oleander GA 2-oxidase 2 mRNA, complete cds.
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/organism="Nerium oleander"
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/db_xref="taxon:63479"
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/note="GAZox2"
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                                                                81 LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArglleGlyProAsn 100
                                                                                                                            101 GlyAspValGlyTrpValGluTyrLeuLeuAsnThrAsnProAspValIleSerPro 120
                                                                                                                                                              434
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                                                                                                                                                                                                                                                             141 IleThralaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160
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Wharayota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
asterids, lamiids, Gentianales, Apocynaceae, Apocynoideae,
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80
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                  375 GGCGATGTTGGTTGGGTCGAATACATTCTCCTGTCAACTACTACTCTGAGTTCAACTACCAC
                                                                                                                                                                                             121 LysSerLeuCysIlePheArgGluAsnProHisHisPheArgAlaValValGluAsnTyr
                                                                                                                                                                                                                                                                               555 ATTCATCCTAGGAACGTTTTCAGTAAACTTCTAATGGACGAAAAGAGTGACTCTGTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            260 LysHisArgValLeuAlaAspThrThrLysSerArgLeuSerWetIleTyrPheGlyGly
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                                                                                 315 AAACAAAAAGCTGGGCCAGCTGATCCTTTTGGCTATGGAAACAAGAAGAAGATTGGACCCAAT
                                                                                                                                                                                                                   161 IleArgGlnArgAsnThrLeuSerArgLeuLysAspGluLysSerAspSerCysPhe
                                                                                                                                                                                                                                                                                                                                                                                        ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeu---AsnArgAsnLeuVal
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1 (bases 1 to 1406)
Ubeda-Tomas, S., Garcia-Martinez, J.L. and Lopez-Diaz, I.
1801ation, characterization and multi-site polyadenylation of
GA 20-oxidases and GA 2-oxidases in Nerium oleander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1032 GATAATAGATTGGTCCTATTTGAGAAAGTTGCAGCC 1067
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Nerium oleander gibberellin 2 ox
AY588978
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                                                                                              1292 bp mRNA linear PLN 29-APR-2004 tabacum GA2ox1 mRNA for gibberellin 2-oxidase 1, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /trānslation="MVVLTKPGIDHFPIVKNCKLSSFFNGVPLIDLSKPNSKNLIVKA
CEEFGFFKVINHSVPTEFITKLESEAIKFFSSPLSEKQKAGPADPFGYGNKKIGPNGD
VGWVEYILLSTNSEFNYHKFASILGVNPETIRAAVNDYVSAVKKMACEILEMLABGLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IHPRNVFSKLLMDEKSDSVFRLNHYPPCPEIQQFSDNNLIGFGEHTDPQIISVLRSNN
TSGLQILLKNGHWISVPPDPNSFPINVGDSLQVMTNGRFKSVRHRVLANSVKSRLSMI
YFGGPPLSEKIAPLASLMEGEESLYEEFTWFEYKKSAYKTRLADNRLVLFEKVAAS"
                                                                                                                                                                                                                                                                                                                                                      Sakane,M., Nakajima,M. and Yamaguchi,I.

Direct Submission

Direct Submission

Direct Submission

Submitted (28-0CT-2003) Masayuki Sakane, University of Tokyo,
Applied Biological Chemistry; Yayoi 1-1-1, Bunkyo-ku, Tokyo

113-0032, Japan (B-mail:m-sakane@pgri.ch.a.u-ckyo.ac.jp,

URL:http://pgrl.ch.a.u-tokyo.ac.jp/, Tel:81-3-5841-5158(ex.25158),

Fax:81-3-5841-8025)
                                                                                                                                                                                         Nicotiana tabacum (common tobacco)
Nicotiana tabacum
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
asterids, lamiids, Solanales, Solanaceae, Nicotiana.
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213
49
68
2
320 AspAsnArgLeuAlaProPheGlnLysSerAlaAla 331
                                                                                                                                                                                                                                                                                         Sakane, M., Nakajima, M. and Yamaguchi, I.
Molecular cloning of GA 2-oxidase in BY-2
Unpublished
2 (bases 1 to 1292)
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Matches:
Conservative:
Mismatches:
Indels:
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/protein_id="BAD17855.1"
/db_xref="GI:46849529"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Nicotiana tabacum"
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/db xref="taxon:4097"
/cell line="BY-2"
1. 11292
/gene="GA2ox1"
75. 1073
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                Gaps:
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78.92%
64.16%
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AB125232.1
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Best Local Similarity:
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Query Match:
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MacMillan, J., Ward, D.A., Phillips, A.L., Sanchez-Beltran, M.J., Gaskin, P., Lange, T. and Hedden, P. Gibberellin biosynthesis from gibberellin Al2-aldehyde in endosperm and embryos of Marah macrocarpus
Plant Physiol. 113 (4), 1369-1377 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLN 01-MAY-1997
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Marah macrocarpus
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I, Cucurbitales, Cucurbitaceae, Marah.
                                                                                                                                                                                                                                                                                                        SerVallysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPhe 277
                                                                                                             118 TACTCCTTTTCATTAATGTTGGTGATTCCTTGCAGGAAATGACTAATGGGAGATTTAGG
                                                                                                                                                                                                                                                                                                                          278 GlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        898 GAAAGTITGIATAAGGAATICACATGGTGTGAATACAAGAAGICAGCTTACAAGAAGACGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (31-0CT-1996) P. Hedden, University of Bristol, Department of Agricultural Sciences, IACR-Long Ashton Research Station, Long Ashton, Bristol, BS18 9AF, UK Location/Qualifiers
                                                 CysPheArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsn---ArgAsn
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/dev_stage="immature seed"
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M.macrocarpa mRNA for dloxygenase.
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/protein_id="CAA70330.1"
/db_xref="GI:1666096"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:48242"
/clone="M7-3"
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KACQEFGFFKVINHGVPLEFITKLEGEAVKFFNLPQPEKEKVRPAKFFGYGNKRIGGN
GDVGWIEYLLLATNPELVYEKAVTIPGDSELFWSCVNDYVSAVRSMACDVLDMIADGL
KIGPRNVLSTLLRDEKSDAVFRLMYPPCFELQALGGRNLIGFGFHTDPQIISVVSN
NYSGLQISLKOGTWAVSVPPDQYSFFINVGDSLQWMTNGRFRSYKHRVFADGLKSRVSM
IYLGGPPLDEKIAPLSSLMEEGGESLYKEFTWCEYKKSAXKTRLGDNRLKFFFEKSVGQ
                  2 (bases i to 1406)
Ubcda-Tomas, Garcia-Martinez,J.L. and Lopez-Diaz,I.
Ubcda-Tomas,S., Garcia-Martinez,J.L. and Lopez-Diaz,I.
Direct Submission
Submitted (02-APR-2004) Instituto de Biologia Molecular de Plantas,
CSIC/Universidad Politecnica de Valencia, Avda de los Naranjos sn,
Valencia 46022, Spain
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CCCTCCACCAACTTCTAGGAAGGAATTCCTGTGATTGACCTCTTCAAACCTGAGGGCAAAC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 AsnLeulleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1406
216
47
65
4
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                     /product="gibberellin 2 oxidase"
/protein_id="AAT72916.1"
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                                                                                                                       1. .1406
/organism="Nerium oleander"
/mol type="mRNA"
/db xref="taxon:63479"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-670-454-2 (1-331) x AY588978 (1-1406)
                                                                                                                                                                                                             gene="GA2ox3"
                                                                                                                                                                                                                                            gene="GA2ox3"
                                                                                                                                                                                                                                                                            codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58e-96
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79.22%
65.06%
64.07%
   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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/tränslation="MAAASSBAAFYSGIPLIDLSAPDAKQLIVKACEELGFFKVVKH
GVPMELISSLESESTRFFSLPLSEKQRAGPPSPFGYGNKQJGRNGDVGWVEYLLLNTH
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DEGSDSVFRVNHYPFCPDLOALKGTMNIGFGEHTDPQIISVLRSNNTSGFQISLADGN
WISVPPDHSSFFINVGDSLQVMTNGFFKSVKHRVLTNSSKSRVSMIYFGGFDISEKIA
                                                                                            976 GGCCACCTITGAGIGAAAAAAAAAGATAGCCCTITACCTICCCTAATG---AAAGGAGAAGAA 1032
                                                                                                                                                       1033 AGTTTGTACAAAGAGTTCACTTGGTTTGAGTACAAGAGATCAGCTTACAACTCTAGGTTG 1092
                                                                                                                                                                                                                                                                                                                     CMA315663 1383 bp mRNA linear PLN 19-JUN-2003
Cucurbita maxima partial mRNA for Gibberellin 2-oxidase (ga2ox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Frisse, A. and Lange, T. Gibberellin biosynthesis in young seedlings of Cucurbita maxima Unpublished
299 CysLeuTyrLysGluPheThrTrpCysGluTyrLysLysAlaAlaTyrThrSerArgLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TU
GERMANY
                                                        GlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGlu
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Matches:
Conservative:
Mismatches:
Indels:
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/organism="Cucurbita maxima"

/mol type="maxNA"

/cultivar="Riesenmelone, gelb ge

/db xref="taxon:3661"

/clone="2beta-WS2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="root tips"
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1. .1383
                                                                                                                                                                                                                                                                                                                                                                          AJ315663
AJ315663.1 GI:32127336
ga2Ox gene; gibberellin 2-oxidase.
Cucurbita maxima (winter squash)
Cucurbita maxima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (19-JUN-2001) Lange
Braunschweig, Mendelssohnstr.
related entry AJ315662.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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/gene="ga2ox"
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                   /db_xref="UniProt/TremBL:004162"
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IAPLPSLMKGBESLYKBFTWFEYKRSAYNSKLADNRLVHFERIAAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           268 ATCGTAAAGGCCTGTGAAGGTTGGATTCTTCAAGGTCATCAACCATGGCGTCCCCATG 327
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ATGGTGGTTTTATCCAAAACCAGAAATCCAACAGTTG-------TCT
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                  64 TCTGCAGCATTCTACTCTGGGATTCCATTGATAGACCTCTCTGCACCAGATGCTAAACAA 123
                                                              243
                                                                                                                                               AsnGlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSer 119
                                                                                                                                                                                        120 ProLysSerLeuCysIlePheArgGluAsnProHisHisPheArgAlaValValGluAsn 139
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                                                                                                                                                                                                                                                           TyrileThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeu 159
                                                                                                                                                                                                                                                                                 483
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                                                                                                                                                                                                                                                                                                                PheArgLeuAsnHisTyrProProCysProGluValGlnAlaLeu---AsnArgAsnLeu 198
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                                                                                                                                 GluLysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArglleGlyPro 99
                                                                                           LeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSer 79
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                                                                                                                                                                                                                                 424 TACATCTCGGCTGTGAGGAACATGGCGGGTGAAATCCTCGAGCTAATGGCGGAAGGGTTG
                                                                                                                                                                                                                                                                                                                                                                                                    SerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299 CysleuTyrLysGluPheThrTrpCysGluTyrLysLysAlaAlaTyrThrSerArgLeu
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s 1292 bp mRNA linear PLN 28-JUL-2004 sativa Ls2ox1 mRNA for gibberellin 2-oxidase No1, complete

AB031206 Lactuca

cds

DEFINITION

LOCUS

AB031206 AB031206.1 GI:9971226 gibberellin 2-oxidase Nol.

ACCESSION VERSION KEYWORDS

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/traislation="Myalskpbirgpppmkpskpntnpl.fptipliblskpeskqhlv
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Lactuca sativa
Bukaryora, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
asterids, campanulids, Asterales, Asteraceae, Cichorioldeae,
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                                                                                                                                                                                                                                                   Toyomasu,T., Mitsuhashi,W. and Kamiya,Y.
Toyomasu,T., Mitsuhashi,W. and Kamiya,Y.
Direct Submission
Submitted (17-AUG-1999) Tomonobu Toyomasu, Yamagata University,
Raculty of Agriculture; Wakaba-cho 1-23, Tsuruoka, Yamagata
997-8555, Japan (E-mail:toyomasu@tds1.tr.yamagata-u.ac.jp,
Tel:81-235-28-2861, Fax:81-235-28-2812)
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Misaminami, K., Sawada, Y., Suzuki, M., Kenmoku, H., Kawaide, H.,
Misahashi, W., Sassa, T., Inoue, Y., Kamiya, Y. and Toyomasu, T.
Deactivation of gibberellin by 2-oxidation during germination
photoblastic lettuce seeds
Blosci. Biotechnol. Biochem. 67 (7), 1551-1558 (2003)
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Lactuca sativa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="Ls2ox1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="Ls2ox1"
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1104.50
78.34%
63.20%
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Best Local Similarity:
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gibberellin

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206
48
58
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1. 1308
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Matches:
Conservative:
Mismatches:
Indels:
  organism="Cucurbita maxima"
                                                                                                                                                                                                           /function="2-oxoglutarate
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1102.50
81.15%
65.81%
63.07%
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Submitted (14-DEC-2000) Lange T., Botanical Institute, Dept. Plant
Physiology and Biochemistry, TU Braunschweig, Mendelsschnstr. 4,
Braunschweig, D-38106, GERMANY
Location/Qualifiers
1.1308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cucurbita maxima bukaryota; Embryophyta; Tracheophyta; Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids; cucurbitales; Cucurbitaceae; Cucurbita.
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                                                                                                                                                                                                                                                                                                    628
                                                                                                                                                                                                                                                                                                                                            SerCysPheArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsn 197
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                                                                                                           689 GGAAGGAAATTAGTGGGTTTCGGAGAACACACAGACCCACAAATCATATCGGTTTTAAGA
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                                                                                    118 IleSerProLysSerLeuCysIlePheArgGluAsnProHisHisPheArgAlaValVal
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Cucurbita maxima mRNA for gibberellin 2-oxidase (ga2ox gene)
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ga2Ox gene; gibberellin 2-oxidase.
Cucurbita maxima (winter squash)
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AspSerCysPheArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArg 196
  GCGAAAACCCGAATCGTAAAAGCCTGCGAGGAGTTCGGGTTCTTCAAGGTCGTAAACCAC 180
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicotyledons;
rosids; eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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                               SerGlyLeuGln11eCysLeuThrAspGlyThrTrpValSerValProProAspGlnThr
                                                                      SerPhePhelleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSer
                                                                                                               VallysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGly
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TCTGGATTTCAAATCTCTCTCTGGAATGGGAATTGGATATCTGTTCCTCCCGATCACAGC
                                                                                    TCCTTCTTCATCATGTTGGTGACTCTTTACAGGTGATGACTAATGGAAGATTCAAAAGT
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Stress-regulated genes of plants, transgenic plants containing same, and methods of use
Patent: WO 0216655-A 1350 28-FEB-2002;
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/organism="Arabidopsis thali
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Sequence 1350 from Patent W00216655.
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Abz13545 Arabidops
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Add60081 Rice gene
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Adz69812 Rice gene
Adx00079 Rice Gone
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Adx19469 Arabidops
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      Phaseolus coccineus
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-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2 1/08FV0 spool/US10670454/runat 27122005 124840 29089/app query.fasta_1.519
-Q=/cgn2 1/08FV0 spool/US10670454/runat 27122005 124840 29089/app query.fasta_1.519
-DB=N Geneseq -QFWT=fastap -SUFTX=p2n.rng -MINWATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -RDE=1 -MATRIX=bits -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-UNITSM==pct -NORM==xct -HEAPSIZE=500 -MINLENE - MAX=10000000
-USER=US10670454 @CGN 11 727 @runat 27122005 124840 29089 -NCPU=6 -ICFU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Database :

Regult . 8

WPI; 2004-758349/74

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New DNA plasmid comprising a T-DNA comprising an Agrobacterium Ti pla first border region linked to a transgene linked to an Agrobacterium plasmid second border region, useful for enhancing production of
                                                                                                                                                                       transgenic plants.
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Example 1; SEQ ID NO 3; 77pp; English.

The present invention relates to a DNA plasmid comprising a transfer DNA (T-DNA) comprising an Agrobacterium Ti plasmid first border region linked to an Agrobacterium Ti plasmid second con transgene linked to an Agrobacterium Ti plasmid second border region, and located in the DNA plasmid outside of the T-DNA is a plant expression cassette comprising a plant cell non-lethal negative selectable marker gene linked to a vector backbone DNA. Also disclosed are a method for enhancing the selection of transgenic plants that do not contain vector backbone DNA, a method for reducing the copy number of a transgene in a plant cell, and a transgenic plant produced by the method. The DNA plasmid comprises the expression cassette comprising a promoter that functions in plant cells operably linked to a plant cell non-lethal negative selection marker gene. The promoter expresses the linked non-lethal negative selection marker gene. The promoter expresses the linked non-lethal negative selection marker gene constitutive promoter. The promoter expresses the linked non-lethal negative selection marker gene of selectable marker gene comprises a plant hormone unitable that calivering gene or signalling gene, or metabolic interference comprises a transgene is a plant positive selectable marker gene selected from gibberellic acid pathway genes. The transgene of agronomic interest. The plant hormone comprises a transgene of agronomic interest. The plant hormone comprises a transgene of agronomic interest. The plant hormone comprises a transgene of agronomic interest. The plant hormone comprises a plant positive selected from gibberellic acid pathway genes, ethylene pathway genes, ethylene pathway genes, ethylene pathway genes, and herbidial selection for commercially viable transgenic pathway genes. The plasmid is useful for enhancing the production of commercially viable transgenic pathway energies a plant positive selectable marker genes electable marker genes electable marker genes electable marker genes electable marker genes ele The sequence is used as a non-lethal negative selectable 2-oxidase.

Sequence 999 BP; 263 A; 221 C; 249 G; 266 T; 0 U; 0 Other;

180 240 100 300 GlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro 120 40 80 9 9 ThrProLeuPheThrGly1leProValValAspLeuThrHisProAspAlaLysAsnLeu GluLeuMet hla AsnieuGlu Asniglu Ala Leu Arg Phe Phely signification GAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLysSer IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn AAAGACAAGAGCTGCTCCCCCGACCTTTCGGCTATGGTAGCAAGAGGATTGGCCCAAAC 1 Argerrerrerereredecagearreaeceaerrerrereraaecearreaaeree 999 331 0 0 0 Length: Matches: Conservative: Mismatches: Indels: Gaps: US-10-670-454-2 (1-331) x ADT62692 (1-999) 2.61e-180 1748.00 100.00% 100.00% Similarity: cal Similarity: 21 181 241 101 47 61 81 best Local S. Query Match: DB: ò g ò ద ર્જ 유 ò a ò g ð

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IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly
                                                      ATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTGATGGCGGAGGGGTTGGG
                                                                                                LeuGlnIleCysLeuThrAspGlyThrTrpValSerValProProAspGlnThrSerPhe
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                                                                                                                                                                                                                                                                                                                                            AlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCysLeu
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/product= "Gibberellin 2.oxidase PcGA2ox1"
/transl_except= (pos:1058. .1063, aa:Ala)
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                                                                                                                                                                                                                                                                                                                                                                                                                                         961 AATAGGCTTGCCCCTTTCCAGAAATCTGCTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inactivation; growth inhibition;
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15-JUL-1998;
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This sequence represents cDNA encoding a runner bean gibberellin (GA) 2-
coxidase, PcGAZOXI. This enzyme is a GA 2-beta-hydroxylase that acts on
C19-GAs and for which 2-beta-hydroxylation is the only activity.
C19-GAS and for which 2-beta position of a GA results in a biologically
inactive product, and is the most important route for GA metabolism in
C2 plants, ensuring that the active hormones do not accumulate in plant
C3 plants. The nucleic acids can be used to transform plants so that
C4 tissues. The nucleic acids can be constitutively over-expressed or otherwise
C5 gibberellin 2-oxidase can be constitutively over-expressed or otherwise
C6 gibberellin 2-oxidase can be constitutively over-expressed or otherwise
C7 character of inhibit plant growth applications such as enhancing lodging-
C8 gircultural and horticultural applications such as enhancing lodging-
C9 agricultural and horticultural applications such as enhancing lodging-
C9 cresistance and grain yield in cereals, improving seedling quality,
C8 and ornamental trees, improving tolerance to cold, drought and infection,
C9 and increasing yields (by the diversion of assemilates from vegetative to
C8 and increasing yields (by the diversion of assemilates from vegetative to
C8 and increasing yields (by the diversion of seeds and reduce shoot
C9 cardox female sterility (by expression in floral organs), prevent pre-
C9 harvest sprouting, reduce shoot growth in hedging plants, inhibit
C9 creversibility in the development or gerwination of geeds and reduce shoot
C9 caids can also be used to transform plants to reduce the expression of GA
C9 caids can also be used to transform plants to reduce the expression of GA
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C9 caids can also be used or transform the captered by the reduce the expression of GA
C9 coxid
                                                                                                                                                                                                  d plant gibberellin 2-oxidase enzymes and nucleic acids, used transgenic plants with improved or altered growth
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P-PSDB; AAY58597.
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Sequence 1318 BP; 358 A; 296 C; 282 G; 382 T; 0 U; 0 Other;

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                                                           IleThralaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly
                                                                                                      PheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsnSerThrSerGly
                                                                                                                                                                                                                                                                                              TIGCAAAICTGICTCCACAGATGGCACTIGGGTITCAGTCCCACCTGATCAGACTTCCTTT
                       368 GGTGATGTCGGTTGGGTCGAATACCTCCTCCTCAACACCCAACCCTGATGTTATCTCACCC
                                             LysSerLeuCysIlePheArgGluAsnProHisHisPheArgAlaValValGluAsnTyr
                                                                                                                                       IleArgGlnArgAsnThrLeuSerArgLeuLysAspGluLysSerAspSerCysPhe
                                                                                                                                                    ArgleuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly
                                                                                                                                                                                                  TTTGGGGAGCACACAGACCCCACAGATATTTCTGTCTTAAGATCTAACAGACACATCTGGC
                                                                                                                                                                                                                                                                                 LeuGlnIleCysLeuThrAspGlyThrTrpValSerValProProAspGlnThrSerPhe
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/note=""Xaa is an unspecified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           product= "gibberellic acid 2-oxidase 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Soybean gibberellic acid 2-oxidase 1 cDNA sequence.
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942 CCACCCTTGTGTGAAAAGATAGCACCTTTACCTTCACTCATGTTAAAAGGAGAAGAGAGT 1001
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402 GGCGATGTCGGTTGGGTCGAATACCTCCTTCTCAACACCCAACCCTGATGTCATCTCCCCC 461
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                                                                            462 AAGTCACAGTTCATTTTCAGAGAAGGTCCTCAGAATTTCAGGGCGGTGGTGGAGGAATAC
                                                                                                                                        582 ATAACGCAGAGGAATGTGTTGAGTTAGGTTGCTGAAGGATGAGAAGAGTGATYCTTGCTTC
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                                                                                                          ileargginargasnThrLeuSerargLeuLeuLysaspGluLysSeraspSerCysPhe
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/note= "Xaa = any amino acid"
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/*tag= a
/product= "GA 2-oxidase 1 protein"
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                                                                                                                                                                                                                   Kishore GM, Logusch EW, Logusch SJ;
                                                                                                                                                                                                                                                                                                                                 Obtaining tranagenic plant useful for controlling seed germination ar seedling growth comprises tranagene comprising a sequence expressing altered levels of an essential hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1359 BP; 340 A; 305 C; 304 G; 409 T; 0 U; 1 Other;
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                 Brown SM, Elich TD,
Piller KJ, Rao S, F
                                                                                                                                                                             (MONS ) MONSANTO CO
                                                                                                                                                                                                                                                                         WPI; 2000-224351/19
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Query Match:
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  WO200009722-A2
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Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
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| IleargGlnargAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe
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(SYGN ) SYNGENTA PARTICIPATIONS AG.
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26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
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                                                                                                                                                                                                                                                                                                                                                                             The invention relates to control of gibberellin (GA) levels in plants.

The method involves producing transgenic plants having a phenotype of reduced seed germination and reduced early seedling growth, then restoring seed germination and early seedling growth by treating plants with an appropriate compound when conditions are favourable. The method is useful to control seed germination and/or early seedling growth in gricultural production so that unfavorable environmental conditions normally reducing agronomic output can be avoided and yields increased. Plants also demonstrate increased uniformity of germination, emergence and seedling vigor, so increasing yields at harvest. The method is especially useful in crop plants such as e.g. canola, soybean, cotton, etc., and is also useful in storage and transport of seeds to reduce premature germination which may affect agronomic or food quality of the seeds. The present sequence is soybean GA 2-oxidase I CDNA
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                                                                                                                                                                                                                                  Control of gibberellin levels in plants useful to avoid unfavorable conditions in crops to increase yields, using transgenic plants having reduced seed germination and early seedling growth then treatment to restore these properties.
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                                                                                                         Logusch EW, Logusch SJ;
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S, Tao
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F, Quan S,
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                             The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell producting a profile of expressed polynucleotides in the plant cell production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
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           + Sequence Listing; English
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The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
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277 PheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGly
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This sequence represents cDNA encoding an Arabidopsis thaliana

CC gibberellin (GA) 2-oxidase, PcGA20x2. This enzyme is a GA 2-beta-

CC gibberellin (GA) 2-oxidase, PcGA20x2. This enzyme is a GA 2-beta-

CC gibberellin (GA) 2-oxidase, PcGA20x2. This enzyme is a GA 2-beta-

CC its only activity. Hydroxylation at the 2-beta position of a GA results

CC GA metabolism in plants, ensuring that the active hormones do not

CC GA metabolism in plants, ensuring that the active hormones do not

CC compulate in plant tissues. The nucleic acids can be used to transform

CC accumulate in plant tissues. The nucleic acids can be used to transform

CC contains so that gibberellin 2-oxidase can be constitutively over-expressed

CC or otherwise enhanced to reduce the concentration of bloactive GAs in the

CC plants and therefore to inhibit plant growth. Growth inhibition is useful

CC plants and increasing yield in Cereals, improving seedling

CC lodging-resistence and grain yield in Cereals, improving seedling

CC clodging-resistence and grain yield in Cereals, improving bloact and

CC clodging-resistence and grain yield in Cereals, improving tolerance to cold, drought and

corchard and onnamental trees, improving tolerance to cold, drought and

corchard and onnamental trees, improving tolerance to cold, drought and

corchard and onnamental trees, improving tolerance to cold, drought and

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corchard and onnamental trees, improving tolerance to cold, drought and

corchard and onnamental trees, improving tolerance of sestiminates from

corchard and onnamental trees, improving tolerance of serving seed and

corchard and onnamental trees, improve shoot growth in commercial wood species. Antisense constructs of

continuous stin texture and fruit shape in apples, increase stem

colery and rhubarb, improve malting yields and quality in cereals

colery and rhubarb, improve malting yields and quality in cereals

colery and rhubarb, improve malting yields and quality 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated plant gibberellin 2-oxidase enzymes and nucleic acids, used to produce transgenic plants with improved or altered growth characteristics.
                                                                                                                                                                                                                                                                                                            Gibberellin 2-oxidase; AtGA2ox2; 2-beta-hydroxylation; inactivation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "Gibberellin 2-oxidase AtGA2ox2"
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317 ArgLeuAlaAspAsnArgLeuAlaProPheGlnLys 328
                                         958 AAGCTTGGTGATTATAGACTTGGTCTCTTTGAGAAA 993
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109. .1134
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98GB-00015404.
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12-JUL-2000; 2000US-00614912
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Lohman KN, Rer
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Shen JB,
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 280 G; 324 T; 0 U; 0 Other;
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Mismatches:
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3-beta hydroxylase, Riboflavin specific deaminase, Ethylene response factor, Acyl-CoA thioesterase II, ABC transporter GCN20-like, Pedyl-CoA thioesterase II, ABC transporter GCN20-like, Pedyl-CoA thioesterase II, ABC transporter and MRP4 ABC transporter. PMPND ABC transporter and MRP4 ABC transporter. PMPND ABC transporter and mRP4 ABC transporter. The nucleic acid fragments may be used to create transgenic plants where the polypeptides are present at higher or lower levels than normal or in cell types or in developmental stages in which they are not normally found. The polymucleotides can be used as probes for genetically and physically mapping genes and as markers for traits linked to those genes. The nucleic acid fragments may be used as restriction fragment length polymorphism (RFLP). It can also be used to probe Southern blots containing restriction endonuclease-treated genomic DNAs of a set of individuals representing parent and progeny of a defined genetic cross. The nucleic acid fragments may also be used trom the mutation problase containing the mutation products generated from the mutation population using the mutation tag sequence primer in conjunction with an arbitrary genomic site primer. The peptides can also be used to immunise animals to produce polyclonal or monoclonal antibodies with specificity for peptides or produce polyclonal or monoclonal attuin cells or in vitro in cell for detecting the polypeptides in situ in cells or in vitro in cell cextracts. The present sequence encodes a plant metabolism protein (or
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Sequence 1352 BP; 439 A; 255 C; 243 G; 415 T; 0 U; 0 Other;

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ATGGTGTTGTTGTTCCAAAGAACAACAAACAATACTCCTACATTAAGAACTGCATGCCA
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1044 TATAAAGAGTTTACCTGGTTTGAGTACAAAAATCAATCTACGGTTCAAGATTATCTAAA 1103
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ndina AR, Sakai H, Weng Z, Caimi PG, Fang Y;
Anderson SL, Shi J, Lu G, Helentjaris TG;
                                                                                                                                      PhelleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLys
                                                                                                                                                                                            HisArgvalLeualaasgThrThrLysSerArgLeuSerMet11eTyrPheGlyGlyPro
                                         TTTGGAGAACACACAGACCCACAAAATCATCTCTGTTAAAGATCCAACAACACTTCAGGC
                                                                               LeuGlnIleCysLeuThrAspGlyThrTrpValSerValProProAspGlnThrSerPhe
                                                                                               TTATTAACGTTGGTGATTCTCTTCAGGTTATGACAAATGGAAGGTTCCGAAGTGTGAGA
                                                                                                                                                                                                                      CACAGAGTGTTGGCAAATGGGTTCAAGTCCAGGCTTTCAATGATTTACTTTGGAGGTCCA
                                                                                                                                                                                                                                                  281 AlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCysLeu
AGGGTGAATCATTACCCTGCTTGTCCTGAAATGACTCTGAATGATCAGAACTTGATTGGG
                           PheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsnSerThrSerGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Soybean; 88; plant; plant metabolism; GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate synthase; Dioxygenase; Ent-Kaurene Synthase A; GA-20 oxidase; Gtorygenase; Ent-Kaurene Synthase A; GA-20 oxidase; Gtorygenase; Ethylene response factor; Acyl-CoA thioseterase II; ABC transporter GTOX20-11ke; Peglycoprotein I; Peglycoprotein 3; Peglycoprotein ATPGF; Peglycoprotein HVMMR2; ABC transporter; PMP70 ABC transporter;
                                                                                                                                                                                                                                                                                                                                                                                         1104 AATAGACTTGAACATTTTGAAAGAATTGCAGCT 1136
                                                                                                                                                                                                                                                                                                                                                              AsnArgLeuAlaProPheGlnLysSerAlaAla 331
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PIONEER HI-BRED INT INC.
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99US-0143412P.
99US-0146650P.
99US-0170906P.
99US-0172946P.
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Lohman KN, Rend
, Zoughi IL, An
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21-DEC-1999;
21-DEC-1999;
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30-JUL-1999;
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Shen JB,
Li CP;
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LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn 100

81

P-PSDB; ADM94206

New isolated GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate synthase nucleic acid and proteins, useful for creating transgenic plants where polypeptides are present at higher or lower levels.

Example 3; SEQ ID NO 5; 186pp; English

The invention relates to an isolated polynucleotide comprising a nucleotide sequence encoding a polypeptide having GTP cyclohydrolase incleotide sequence encoding a polypeptide having GTP cyclohydrolase [1/3,4-dihydroxy-2-butanone-4-phosphate synthase activity, appearing a coll with the comprising the polynucleotide operably linked to at least one regulatory sequence, transforming a cell with the comprising the recombinant DNA construct.

The polynucleotide and resentatory sequence, transforming a plant cell with the polynucleotide and resentant of the recombinant DNA construct and a seed comprising the recombinant DNA construct and a seed comprising the recombinant DNA construct and a seed comprising the recombinant DNA construct. Also disclosed as new are nucleic acid the recombinant DNA construct. Also disclosed as new are nucleic acid the recombinant DNA construct. Also disclosed as new are nucleic acid the recombinant DNA construct. Also disclosed as new are nucleic acid consent and assembled contigs encoding plant metabolism proteins chosen from GTP cyclohydrolase [1/3,4-dihydroxy-2-but amporter]. Also disclosed as new are nucleic acid consent and assembled contigs encoding plant metabolism proteins chosen from GTP cyclohydrolase. Nucleus PNA CONSTRUCT AND CONSTRU fragment)

Sequence 1365 BP; 448 A; 258 C; 244 G; 415 T; 0 U; 0 Other;

MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLysSer 20 ThrProLeuPheThrGlylleProValValAspLeuThrHisProAspAlaLysAsnLeu 40 |||||||||:::|||||||::: ATGGTGTTGTTGTCCAAAGAACAACAAACAATACTCCTACATTAAGAACTGCATGCCA 1365 200 57 69 5 Conservative: Mismatches: Indels: Length: Matches: US-10-670-454-2 (1-331) x ADM94205 (1-1365) 3.42e-105 1060.50 77.64% 60.42% 60.67% Similarity: Percent Similarity: Best Local Similari Alignment Scores: Pred. No.: 21 Query Match: DB: ò 셤 ð g ò

61

g å 셤

/product= "gibberellic acid 2-oxidase 2" Location/Qualifiers 149. .1129 BP AAZ99472 standard; cDNA; 1403 (first entry) 03-JUL-2000 Glycine max. 321 AAZ99472 පු 8 346 GAAGCTATATCCGAATTGGAATATGAAGCCTTCAAATTCTTCTTCTATGTCACTCAATGAA 405 41 IlevalAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60 GluteuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80 286 ATAGTGAAGGCTTGTGAGGAGTTTGGATTCTTCAAAGTCATCATGGTGTCTCCATG

994 CCTTTGAGTGAGAAAATAGCACCATTATCCTCTCTCATG---AAAGGAAAAGAAAGTCT 1050 753 220 240 873 PhelleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLys 260 HisargvalLeuAlaAspThrThrLysSerArgLeuSerMet11eTyrPheGlyGlyPro 280 281 AlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCysLeu 300 TyriysGluPheThrTrpCysGluTyriysiysAlaAlaTyrThrSerArgieuAlaAsp 320 693 200 813 933 CACAGAGTGTTGGCAAATGGGTTCAAGTCCAGGCTTTCAATGATTTACTTTGGAGGTCCA 993 101 GlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro 120 121 LysSerLeuCysllePheArgGluAsnProHisHisPheArgAlaValValGluAsnTyr 140 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160 LeuGlnileCysLeuThrAspGlyThrTrpValSerValProProAspGlnThrSerPhe TTTGGAGAACACACAGACCCACAAATCATCTCTGTTAAGATCCAACAACACTTCAGGC IleargGlnargasnThrLeuSerArgLeuLeuLysaspGluLysSerAspSerCysPhe ArgieuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly PheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsnSerThrSerGly Gibberellic acid; copalyl diphosphate synthase; 3beta-hydroxylase; 2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase; seed germination; seedling growth; gibberellin biosynthetic pathway; transgenic plant; hypocotyl; epicotyl; se. 466 AGGGACGTTGGTTGGATTGAGTACCTTCTTCTCAACACCAATCAGAA---Soybean gibberellic acid 2-oxidase 2 cDNA sequence. 1111 AATAGACTTGAACATTTGAAAGAATTGCAGCT 1143 AsnArgLeuAlaProPheGlnLysSerAlaAla 301 141 161 634 694 754 814 241 874 261 181 201 221 셤 요 ò 셤 ò 셤 ò 셤 8 셤 ઠે 셤 ò 셤 ð a ò 셤 ò 셤 ઠે 셤 ઠ

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1031 TACAAAGAGTTTACGTGGTTCGAGTATAAAATTTAACCTATGCTTCAAGATTGGCTGAT 1090
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                            496
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                                                                                                       TTTGGAGAACACACACACACAAATCATTTCTCTACTTAGGTCCAACAATACTTCAGGC
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449 GGGGATGTTGGTTGGGTTGAGTACCTTCTTCTCAACACCCAATCAAGAA-
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'product= "GA 2-oxidase 2 protein"
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149. .1129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 ileValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Obtaining transgenic plant useful for controlling seed germination and seedling growth comprises transgene comprising a sequence expressing altered levels of an essential hormone.
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                                                                                                                                                                                                                                                                                                     Kishore GM, Logusch EW, Logusch SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1403 BP; 440 A; 269 C; 261 G; 433 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 45; Page 250; 267pp; English
                                                                                                                                                                                                                                                                                                Heck GR,
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                                                                                                                                                                                                                                                                                                                            Ream JE;
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compared to normal plants
                                                                                                                                                                                                                                                                                                Elich TD,
                                                                                                                                                                                                                                                                                                                                                                           2000-224351/19.
                                                                                                                                                                                                                                                  (MONS ) MONSANTO CO
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                              WO200009722-A2
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Percent Similarity:
                                                                                                                                                                            10-AUG-1998;
                                                                                                                           10-AUG-1999;
                                                                                                                                                                                                 07-JUN-1999;
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                                                                                                                                                                                                The invention relates to control of gibberellin (GA) levels in plants.

The method involves producing transgenic plants having a phenotype of reduced seed germination and reduced early seedling growth, then restoring seed germination and early seedling growth by treating plants with an appropriate compound when conditions are favourable. The method is useful to control seed germination and/or early seedling growth in apropriate compound when conditions are favourable. The method is agricultural production so that unfavorable environmental conditions normally reducing agronomic output can be avoided and yields increased. Plants also demonstrate increased uniformity of germination, emergence and seedling vigor, so increasing yields at harvest. The method is especially useful in crop plants such as e.g. canola, soybean, cotton, etc., and is also useful in storage and transport of seeds to reduce to premature germination which may affect agronomic or food quality of the seeds. The present sequence is soybean GA 2-oxidase 2 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |||| ::::: ||||||||:::|||||||| GAAACTATGGAATCTGAAGCCTTCAAGAGTTCTTCTCTATGCCACTCAATGAG 388
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                                                                                                                  Control of gibberellin levels in plants useful to avoid unfavorable conditions in crops to increase yields, using transgenic plants having reduced seed germination and early seedling growth then treatment to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro
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ATGGTGTTGCTGTCCAAGGCAACAACAATACTCCTACATCAAGAACTACATGCCA
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                                             Logusch EW, Logusch SJ;
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                                              Heck GR,
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                                                           Ream JE;
 99US-00371307
                                                                                                                                                      restore these properties.
                                              Elich TD,
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                                                           Rao S,
                       (BROW/) BROWN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity:
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                                                                                                                                                                  PhelleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLys
                                                                                                                                                                                                                                                                                                                                                                                                                     TTCATAAATGTTGGTGATTCTCTTCAGGTTATGACCAATGGAAGGTTTCGAAGTGTAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyPro
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                                                                                    ArgleuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly
                                                                                                                                                                                                                             PheglyGluHisThrAspProGlnIleIleSerValLeuArgSerAsnSerThrSerGly
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                                                               IleargGlnargasnThrLeuSerargLeuLysaspGluLysSeraspSerCysPhe
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T, Zou
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Zhu T,
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Whitham S, Xie Z,
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Katagiri F, Quan S,
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The invention relates to a DNA encoding a plant protein having applored in 2-oxidation activity, comprising ADK000079 or ADK00081 or a DNA encoding a protein comprising ADK000800r ADK00082, where one or more amino acid residues are substituted, deleted, added, and/or inserted or DNA hybridising to ADK00079 or ADK00081 under stringent conditions. The DNA is also selected from an antiseane RNA, a DNA encoding an RNA having the ribozyme activity that specifically cleaves the transcript of the DNA above, a DNA encoding an RNA that suppresses the expression of the DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New DNA encoding plant-derived proteins having gibberellin 2-oxidation activity, useful for the inactivation of plant gibberellins and plants whose gibberellin activity has been modified by regulating the expression
                                                                                                                              TyrPheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLys 295
                                                                                                                                              TACTTTGGAGGCCACCGTTAGCACAGAGGATTGCACCATTGCCACAGCTGCTGGGGAG
                                                                                                                                                                                                      TTCAAGAGCGTGAAGCACAGGGTGGTGGCCAACAGCCTAAAGTCTAGGGTTTCCTTCATC
                                                                                                                                                                                       GlyGluGluCysLeuTyrLysGluPheThrTrpCysGluTyrLysLysAlaAlaTyrThr
                            AspGlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArg
                                                                      PhelysSerVallysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIle
                                                                                                                                                                                                                                                                                                                                                                                                                                               Rice, 88; gene; plant; gibberellin 2-oxidase; OsGA20x3; plant growth; gibberellin A20; gibberellin A29; gibberellin A29
                                                                                                                                                                                                                                              SerArgLeuAlaAspAsnArgLeuAlaProPheGlnLys 328
                                                                                                                                                                                                                                                                    TCAAGGCTTGGAGACAACAGGCTGGCCCAGTTTGAGAAG 978
                                                                                                                                                                                                                                                                                                                                                                                                                     Rice cDNA encoding gbiberellin 2-oxidase, OsGA2ox3
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(BIOO-) BIO-ORIENTED TECHNOLOGY RES ADVANCEMENT.
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                                                      involved in plant resistance or response to pathogenic infection. Mi comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (MI) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
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                                          present invention relates to a method (M1) for identifying
                                                                                                                                                                                                    Sequence 984 BP; 165 A; 311 C; 341 G; 167 T; 0 U; 0 Other;
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72.67$
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illustrate the invention.
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Sakamoto

Saito T,

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the expression of the DNA above in plant cells by co-suppression. Also included are a protein encoded by the DNA above, a vector harbouring a DNA selected above, a transformed plant cell harbouring the DNA above or the vector, a transgenic plant cell harbouring the DNA above or the vector, a transgenic plant comprising the transformed plant cell or obtained from the transgenic plant, a propagation material plant, a plant growth suppression comprising the DNA above as an active pranction, a method of suppressing plant growth and a method of promoting plant growth. The gibberellin 2-oxidase catalyses the conversion of gibberellin A29, which is further metabolised to gibberellin A29. Which is further inactivation of plant gibberellin and plants whose gibberellin activity has been modified by regulating the expression of these DNAs. The present sequence encodes gibberellin 2-oxidase, OsGA20x3.
  DNA encoding an RNA that suppresses
  or a
  plant cells via RNAi,
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     apove
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Sequence 984 BP; 165 A; 311 C; 341 G; 167 T; 0 U; 0 Other;

			19	09	39	120	59	180	79	240	66	300	115	360	135	399	155	459	175	519	195	579	215	639	235
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	ttive:		GlnPh	CACAT	Asple	GACCT	PheLy	TCAA	LeuAr	CGTCAG	GIYTY	GGGTA	LeuAs	CTCGC	ArgGl		MetCy	GTGGC	Treuse	SCTGAG	ProCy	SCCGTG	ProG1	SCCGC.	AspGl
	Length: Matches: Conservative Mismatches: Indels: Gaps:	_	LeuAsr	CGTCGA	Valva]	GTCGTC	GlyPhe	GGGTTC	GluAla	GAGGC	ProPhe	ccGTTC	Leule	CICCIC	IlePhe	GTC:	Lysası	CGGAAC	AsnTh	GACGC	TyrPro	TACCC	Thrast	ACCGAC	LeuTh
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759
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                                                            256 PhelysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetile
                                              AspGlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArg
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ki J, Ishikawa
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ta T, Kawakami N, Yazaki J,
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DOKURITSU GYOSEI HOJIN RIKAGAKU KENKYUSH.
ZH KOKUSAI KAGAKU SHINKO ZAIDAN.
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Kawai J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate synthase nucleic acid and proteins, useful for creating transgenic plants where polypeptides are present at higher or lower levels.
                            696
                                                           295
                                                                                                                      GlyGluGluCygLeuTyrLygGluPheThrTrpCygGluTyrLygLygAlaAlaTyrThr 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated polynucleotide comprising a nucleotide sequence encoding a polypeptide having GTP cyclohydrolase 11/3,4-dinydroxy-2-butanone-4-phosphate synthase activity, appearing as ADM94266. Also included are a vector comprising the polynucleotide, a recombinant DNA construct comprising the polynucleotide operably linked to at least one regulatory sequence, transforming a cell with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ', Rafalski JA, Orozco EM, Miao G, Famodu OO;
Rendina AR, Sakai H, Weng Z, Caimi PG, Fang Y;
Anderson SL, Shi J, Lu G, Helentjaris TG;
                                                           TyrPheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLys
                PhelysSerVallysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIle
                                                                                                                                                                                                                                                                                                                                                                                                   Rice; 88; plant; plant metabolism;
GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate synthase;
Dioxygenase, Ent-Kaurene Synthase A; GA-20 oxidase;
Gibberellin 3-beta hydroxylase; Riboflavin specific deaminase;
Ethylene response factor; Acyl-CoA thioesterase II;
ABC transporter GGN20-1ike; Peglycoprotein I; P-glycoprotein 3;
P-glycoprotein ATPGP; P-glycoprotein HVMNR2; AGC transporter;
PMP70 ABC transporter;
                                                                                                                                                                                                     1090 TCAAGGCTTGGAGACAACAGGCTGGCCCAGTTTGAGAAG 1128
                                                                                                                                                                                  SerArgLeuAlaAspAsnArgLeuAlaProPheGlnLys 328
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99US-0143412P.
99US-0146650P.
99US-0170906P.
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Lohman KN, Ren
, Zoughi IL, A
                                                                                                                                                                                                                                                                                                                                                                        Rice Dioxygenase cDNA.
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Shen JB,
Li CP;
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progruction a plant (comprising transforming a plant cell with the producing a plant (comprising transforming a plant cell with the producing a plant (comprising transforming a plant from the transformed plant cell), a plant comprising the recombinant DNA construct. And a snew are mucleid acid the recombinant DNA construct and a snew are mucleid acid construct. And comprising plant metabolism proteins construct from GTP cyclophydrolase II/3,4-dihydroxy-2-buteanone-4-phosphate Synthase, Dioxygenase, Ent-Kaurene Synthase, Ethylene response actors, Acyl-Cob thiosesterase II, ABC transporter GRAPG-like, P. Glycoprotein I. P-Glycoprotein 3, P-Glycoprotein AFEGP, P-Glycoprotein I. P-Glycoprotein 3, P-Glycoprotein AFEGP, P-Glycoprotein GTP mucleic acid fragments may be used to create transgenic plants where the polypeptides are present at higher or lower levels than normally cell types or in developmental stages in which they are not normally controlly mapping genes and as markers for traits linked to those genes. The nucleic acid fragments may be used as probes for genetically and physically mapping genes and as markers for traits linked to those genes. The nucleic acid fragments may be used as restriction fragment length containing restriction endonuclease-traited genomic DNAs of a set of individuals representing parent and progeny of a defined genetic cross. The nucleic acid fragments may also be used as hybridisation probes against PCR amplification products generated from the mutation mopulation using the mutation tag sequence primer. The peptides can also be used to immuniae animals to produce senonic bid minimals and progeny of a defined genetic cross against be mutation transmay also be used as hybridisation probes against to many products generated from the mutation many products generated from the mutation many products generated from the mutation many products are products or mutation which an arbitrary products and progeny of a defined genetic cross and products generated from the mutation products and pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genomic site primer. The peptides can also be used to immunise animals to produce polyclonal or monoclonal antibodies with specificity for peptides or proteins comprising the amino acid sequences. Antibodies are useful for detecting the polypeptides in situ in cells or in vitro in cell extracts. The present sequence encodes a plant metabolism protein (or
        comprising the recombinant DNA construct
    polynucleotide, a cell
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Sequence 1650 BP; 353 A; 463 C; 476 G; 358 T; 0 U; 0 Other;

			ervative: 52	Mismatches: 79		
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ores:	-	σ	larity: 72.67%			12
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US-10-670-454-2 (1-331) x ADM94203 (1-1650)

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1007 GGAGAGCCAGTACAAGGAGTTCACATGGGATGAGTACAAGAAGGCTGCCTACAAA 1066
156 AlaGluGlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLysAspGluLys 175
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                                                        SerAspSerCysPheArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsn
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Run

Scoring table:

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HTC; GSLT CDNA.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyea; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases 1 to 1362)

Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,

Menard, M., Cruaud, C., Quetler, F., Scarpelli, C., Schacher, V.,

Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.

Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:

A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CNSOABSJ 1362 bp mRNA linear HTC 06-FEB-2004 Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTPGH78ZH09 of Hormone Treated Callus of strain col-0 of Arabidopsis thaliana (thale cress).
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Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length librairies construction : Temple G.
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2 (bases 1 to 1362)
  Annotation
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The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length libraties construction: Temple G.

Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,
Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
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                                           699 GTGAAGGTGGGGTTTGGGGAACACACACACACAGATAATCTCAGTGCTAACATCAAT
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          197 AsnLeuValGlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsn
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Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein the June 2003).
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Direct Submission

Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length librairies construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Cleptet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTFB20ZE08 of Flowers and buds of strain col-0 of Arabidopsis thaliana (thale cress).
                                                                942 TTCGGCGGACCGCCATTGAGCCAGAAGATCGCACCATTGCCATGCCCTGTCCCTGAGCAA 1001
                                                                                                                                                1 (bases 1 to 1141)
Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,
Menard, M., Craud, C., Quetier, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J., and Salanoubat, M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
    882 AAGAGTGTTAAACACAGGGTCTTAGCCGATACAAGGAGATCGAGGATTTCAATGATATAT
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Arabidopsis thaliana (thale cress)
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Deery Match: 62.274 Indels: 5 3	#85 AAGAGTGTFAAACACAGAGTCTTAGCCGATACAAGGAGTTTCAATGATATAT 911 277 PheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLygGly 296

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Direct Submission

Submitted (18-NoV-2003) Genoscope - Centre National de Sequencage :

Submitted (18-NoV-2003) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G.

Genoscope members carried out sequencing and annotation : Castelli V. Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGV INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Wunich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
            Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetler, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weisenbach, J. and Salanoubat, M., Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
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http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
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1339 bp mRNA linear HTC 06-FEB-2004
Abbidopesis thaliana Full-length CDNA Complete sequence from clone
GSLTFB70ZF11 of Flowers and buds of strain col-0 of Arabidopsis
thaliana (thale cress).
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HTC; GSLT. CDNA.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Arabidopsis thaliana

Bukaryota, Viridiplantee, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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SerGlnSerGluLysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArg
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                                             GlyValProLeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPheLysLys
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Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University of
Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA

If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB and may be found by BLAST
searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
maize cDNA sequences is either Virginia Walbot, Stanford or Pat
Schnable, Iowa State, then clones may be requested from ZmDB:
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                                                                                                                                                                                                                                                                                                                                                                               /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 LeulleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValPro
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                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="MaizeGDB:638751"
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/organism="Zea mays"
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Mexaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1554)
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Fang, Z., Morgante, M., Landewe, T., Fengler, K., Useche, F.,
Hanafey, M., Tingey, S., Chou, H., Wing, R., Soderlund, C. and Coe, E.H.
                    VallleSerProLysSerLeuCysIlePheArgGluAsnProHisHisPheArgAlaVal 136
                                      940 TTCGGCGGACCGCCATTGAGCCAGAAGATCGCACCATTG-------
                                                                                                                  AsnLeuValGlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsn
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                                                                                            ValGluAsnTyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAla
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Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V. Maize Mapping Project/DuPont Consensus Sequences for Design (Overgo Probes Unpublished (2002)
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/db_xref="taxon:3702"

/clone="GSLTRB56ZG10"

/tissue_type="Flowers an
/ecotype="Col-0"

/plasmid="pcnvSPORT_6"

complement(1. .1128)
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The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
URGY INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
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HTC; GSLT. CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 1128)
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Solanum tuberosum (potato)
Solanum tuberosum
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamilds; Solanales; Solanaceae; Solanum.

E. I (bases Ito 893)
S. Flinn, B., Rothwell, C., Sardana, R., Griffiths, R., Lague, M., De
Koeyer, D., Audy, P., Goyer, C., Li, X.-Q., Wang-Pruski, G. and Regan, S.
Generation of ESTs from late blight-challenged potato tubers
Unpublished (2005)
Contact: Barry Flinn
The Canadian Potato Genome Project - BioAtlantech
921 College Hill Rd, Fredericton, ON, E3B 629, CANADA
Email: bflinn@bioatlantech.nb.ca
Seq primer: T3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                893 bp mRNA linear EST 15-MAR-2005
50141.1 Late Blight-Challenged Tubers Solanum tuberosum cDNA clone
DN589159
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                                                                                                                                                                                                                                         LysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetileTyr 276
117 VallleSerProLysSerLeuCysIlePheArgGluAsnProHisHisPheArgAlaVal 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GluGlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSer
                                                                                                                                                                AsnLeuvalGlyPheGlyGluHisThrAspProGlnIleIleServalLeuArgSerAsn
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                                                                     ValGluAsnTyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAla
                                                                                        GlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPhe
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/mol_type="mRNA"
/cultivar="Shepody"
/db_xref="taxon:4113"
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AJ803092 Antirrhinum majus whole plant Antirrhinum majus CDNA clone
AJ8033092
                      787
                                                     274
                                                                           788 AGGITCAAGAGCGIGAGGCATAGGGTTTTAGCTCACTGTAAAAAATCTAGGGTTTCTATC 847
                                                                                                                           lleTyrPheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeu 294
                                                                                                                                               Antirrhinum majus
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
asterids, lamiids, Lamiales, Plantaginaceae, Antirrhineae,
Antirrhinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 IleGlyProAsnGlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAsp 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 ATTGGACGCAATGGCGATGTGGGATGGCTCGAATACTTGCTCCTAAACACTAAATCTGAT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 SerGlnSerGluLysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArg 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bey, M., Stueber, K., Fellenberg, K., Schwarz-Sommer, Z., Sommer, H., Saedler, H. and Zachgo, S. Antirrhium Petal Development and Characterization of Antirrhium Petal Development and Identification of Target Genes of the Class B MADS Box Gene
CCGGATCACACTTCCTTCTTCAACGTTGGTGACTCTCTCCAGGTGATGACAAATGGG
                                                       ArgPheLysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMet
                                                                                                                                                                                                   LysGlyGluGluCysLeuTyrLysGluPheThrTrpCysGluTyrLysLysAlaAlaTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
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/db_xref="taxon:4151"
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/clone_lib="Antirrhinum majus whole plant"
                                                                                                                                                                                                                                                                                             968 AACTCTAGATTGTCTGATAATAGGCTTCAACAATTCGAAAGG 1009
                                                                                                                                                                                                                                                                         315 ThrSerArgLeuAlaAspAsnArgLeuAlaProPheGlnLys 328
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169
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Matches:
Conservative:
Mismatches:
Indels:
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Molekulare Pflanzengenetik
MPI fuer Zuechtungsforschung
Carl-von-Linne Weg 10, D-50829, Germany.
Location/Qualifiers

    .785
    /organism="Antirrhinum majus"

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Plant Cell 16 (12), 3197-3215 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-670-454-2 (1-331) x AJ803092 (1-785)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antirrhinum majus (snapdragon)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AJ803092.1 GI:51118420
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902.50
81.30%
68.70%
51.63%
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                      728
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792 bp mRNA linear EST 18-OCT-2001
EST55524 tomato flower, anthesis Lycopersicon esculentum cDNA
Clone CTOD23D23 5' end, mRNA sequence.
E1935635
                                                                                                                                                                                                                                                                                                                                                     Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bernatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.

(bases 1 to 792)

van der Heeven, R.S., Bezzerides, J.L., Karamycheva, S.A., Tsai, J.,

van der Heeven, R.S., Ronning, C.M., Nierman, W., Fraser, C.M.,

Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.

Generation of ESTs from tomato flower tissue, anthesis (2001)
ThrTrpCysGluTyrLysLysAlaAlaTyrThrSerArgLeuAlaAspAsnArgLeuAla 324
                                      663 ACATGGTTTGAGTACAAAATTCAGCATATAAATCTAGATTGGCTGATAATAGGTTGGTC 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev stage="anthesis"
/clone lib="tomato flower, anthesis"
/clone lib="tomato flower, site l: Stite l: Scori; Site 2:
/note="Vector: pBluescript SK(-); Site l: EcoRI; Site 2:
Xho!; supplier: Cornell University; sequencing: The
Institute for Genomic Research; Flower buds and flowers
were taken from greenhouse plants (4-8 wks old, TA496).
They were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLysSer
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                                                                                                                                                                                                                                                                                                                                    Lycopersicon esculentum (Solanum lycopersicum)
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158
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42
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116
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1. 792
/organism="Lycopersicon esculentum"
/mol type="mRNA"
/cultivar="TA496"
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/clone="cTOD23D23"
/tissue_type="flower"
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723 CTATTTGAGAAA 734
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                                                                                    ð
                                                          /clone_libe_"Late Blight-Challenged Tubers"
//clone_libe_"Late Blight-Challenged Tubers"
//clone_libe_"Late Blight-Challenge Tubers |
Site 2: Xho1; supplier: Pathogen-challenge series. Tubers |
Incompathogen.free Solanum tuberosum var. Shepody, clone |
1756, were inoculated with 5 ul of Phytophthora infestans (A2-mating type), through 2 puncture wounds 3 cm apart. The tubers were incubated 1 minute to allow inoculum absorption. The infection area was outlined for future collection reference. Surface slices were sampled from the tubers at 1 day, 5 days, 7 days, 11 days and 14 days post-infection. All samples were pooled and used for RNA isolation and library construction. A normalized library was constructed following a modified protocol of Bonaldo et al. (1996. Genome Research 6: 791-806)."
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63 TACATTCTTTTGTCAACAAATTCTGAGTTCAATTACCAAAAATTTGCATCTATTTTGGGT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CysPro---GluValGlnAlaLeuAsn---ArgAsnLeuValGlyPheGlyGluHisThr 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              893
1168
227
33
3
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                     /tissue_type="Tubers"
/lab_host="XL10-Gold"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     x DN589159 (1-893)
                                                                                                                                                                                                                                                                                                                                                                                                                  1.02e-91
868.50
79.92%
68.85%
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Best Local Similarity:
Query Match:
DB:
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/ CLOUE="Vector: palescript II SK+; Site I: ECORI; Site_2:
XhoI; The CDNA library was constructed from mRNA isolated
from unexpanded leaves and the shoot tips of 2 week old
seedling from the cultivar Williams. The 2 week old
seedlings were salt stressed in a solution of 500mM NaCl
for 3 days prior to harvesting. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The CDNA fragments were
directionally cloned into the ECORI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments were
transformed into blub host cells (GibcoBR). This library
was constructed in the laboratory of Dr. Randy
                   Tel: 314 286 1800

Fax: 314 286 1810

Bmail: estewatson.wustl.edu

Bmail: estewatson.wustl.edu

When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com) High quality sequence stopp: 426.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 GAGTTCATGGCCAATTTGGAAAACGAAACCTCAGGTTCTTCAAAAAACCTCAGTCCGAC 257
                                                                                                                                                                                                                                           /organism="Glycine max"
/mol type="mRNA"
/cultivar="Williams"
/cultivar="Williams"
/clone="SOYBEAN CLONE ID: Gm-cl066-4957"
/tissue type="Leaf and shoot tip, salt stressed, 2 week
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 ACGCCCCTGTTCTCCCGGGATTCCCGTGGTCGACCTCACGGACCCCGATGCCAAGACCCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 ATGETTETTTGTCTCAGCCAGCATTAAACCAGTTTTTCCTTCTGAAAACATGCAAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu
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  Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        566
159
19
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Matches:
Conservative:
Mismatches:
Indels:
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/clone_lib="Gm-c1066"
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86.89%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, R., Steptoe, M., Theising, B., Allen, M.,
Schurk, R., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
McCann, R., Waterston, R., and Wilson, R.,
Public Soybean EST project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                               140
                                                                                                                                      LysAspargalaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn 100
                                                                                                                                                                   512
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                                                                                           212
                                                                                                                                                                                                                                    GlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro 120
                                                                                                                                                                                                                                                                                                                                                                        AAATTTGCATCTATATTAGGTGTCAATCCAGAAAACATTCGGGCTGCGGTTAATGATTAT 392
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                                             GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu
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Public Soybean EST Project
Washington University School of Medicine
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VERSION
KEYWORDS
SOURCE
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DEFINITION
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JOURNAL
COMMENT
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77 40 197

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mRNA sequence.
BI208568
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BI208568
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Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Rhanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R., and Wilson, R., Jackson, Y., Cardenas, M.,
WcCann, R., Waterston, R., and Wilson, R.,
Unpublished (1999)
Other ESTS: BU544870 corresponding to Gm-r1088-979 (3')
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Gm-cl023"
/clone_lib="Gm-cl023"
/note="Vector: pSPORTI; Site_1: SalI; Site_2: NotI; This cDNA library was constructed_from mRNA isolated from seed coats (100-200mgs) of greenhouse grown plants. The library was prepared using the Life Technologies pSuperScript cDNA library construction kit. Complimentary DNA was synthesized from mRNA using a poly (dT) sequence with a Not I restrictions site. Sal I linkers adapers were ligated to the blunt-ended cDNA fragments followed by Not I digestion. The CDNA fragments were directionally cloned into the Not I -Sal I restriction site of the pSPORTI vector. The ligated cDNA fragments were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Insert Length: 1472 Std Error: 0.00
High quality sequence stop: 436.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                       AW184969 153 Dp mRNA linear EST 24-JUL-2004 se84f09.yl Gm-c1023 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1023-1410 5' similar to TR:O04162 004162 DIOXYGENASE.;, mRNA
                                                                               497
                                                                                                                         161 IleArgGlnArgAsnThrLeuSerArgLeuLysAspGluLysSerAspSerCysPhe 180
                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
378 AAGTCACAGTTCATTTTCCGAGAAAGTCCTCAGAATTTCAGGGTGGTCGTTGAGGAGTAC 437
                                       /db_xref="taxon:3847"
/clone="GRNOMS SYSTEMS CLONE ID: Gm-c1023-1410"
/tissue_type="seed coats of greenhouse grown plants"
/lab_host="DH10B"
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/cultivar="T157"
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transformed into E.coli Electromax DH10B host cells. Th library was constructed by Dr. Lila Vodkin and Dr. Anu Khanna."

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BI208568 GTOS Lycopersicon esculentum cDNA clone CTOS17020 5' end,
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Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 694)
van der Hoeven,R., Sun,H., Bezzerides,J., Cho,J., Utterback,R.,
Ronning,C. and Tanksley,S.
Generation of ESTS from Tomato Suspension Cultures
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 IleThralaValiysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160
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                                                                                                                                                                                                                                                                                                                                                                                   144 ACGCCCTTGTTCGCGGGGATTCCTGTGGTCGACCTCACGGACCCCGATGCCAAGACCCAC 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 ATAGTCAATGCCTGCAGGGACTTCGGCTTCTTCAAGCTCGTGAACCACGGTGTTCCGTTA 263
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                                                                                                                                                                                                                                   MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324 AAAGACAGGGCTGGTCCCCTGACCCTTTTGGCTACGGCAGCAAGAGGTTGGCCCTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       384 GGGGATGTGGGTTGGGTCGAATACCTCCTTCTCAACACCAACCCTGATGTCATCTCCCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             504 ATTAGAGCGGTGAAGAACATGTGCTATGAGGTGTTGGAATTGATGGCTGANGGATTGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 564 ATAACGCATAGGAATGTGTTGAGTATGTTGCTGAACGATGAGAAGAGTGATTCTTGCTTC
                                                                                                                                                                                                                                                                                                                                    Thr Proteu Phe Thr Glylle Proval Val Aspleu Thr His ProAspAlaLys Asn Leu
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     Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                  (1-653)
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                                                                                                                                                                                  x AW184969
8.09e-86
817.00
84.74%
83.16%
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629

602

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EST 27-APR-2005
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1 (Dases 1 to 755)
Strugne, T., Watanabe, M., Yano, K., Suzuki, H., Sakurai, N. and Shibata, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 ATCGTTAATGCCTGCGAAGAATTCGGATTCTTCAAAATCATAAACCATGACGTTCCTATG 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 IleValAsnAlaCysAzgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
                                                                                                                                                                                                                                  BW690134 Lycopersicon esculentum cv. Micro-Tom fruit Lycopersicon esculentum cDNA clone FC17CG04 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4081"
/clone="FC17CG04"
/tinsue type="fruit"
/clone_lib="Lycoperation esculentum cv. Micro-Tom fruit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLysSer 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expressed sequence tags of full-length cDNA clones prepared from the laboratory-grown miniature tomato (Lycopersicon esculentum) cultivar Micro-Tom miniature tomato (Lycopersicon esculentum) the laboratory-grown miniature tomato (Lycopersicon esculentum) cultivar Micro-Tom Unpublished (2005)

Contact: Daisuke Shibata
Kazusa DNA Research Institute;
7-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan Tel: 81-438-52-3948
Fax: 81-438-52-3948
Exa: 81-438-52-3948
Email: shibatackazusa.or.jp.
Location/Qualifiers
                                       543 TCAAGACTATCAATGATATTTTTGGAGGACCACCATTGAGTGAAAGATAGCACCATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 ACCTCATTCTTTAATGGTGTTCCATTGATTGACCTCTCTAAACCGGACTCCAAGAACCTC
                                                                                                                                                                                                                                                                                                                     Lycopersicon esculentum (Solanum lycopersicum)
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Mismatches:
Indels:
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Matches:
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/mol_type="mRNA"
/cultivar="Micro-Tom"
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798.00
73.36%
57.92%
45.65%
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Pred. No.:
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                                                                                                                                                                               RESULT 14
BW690134
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                                                                                                                     /organism="Lycopersicon esculentum"
/mol type="mRNA"
/culcivar="TA456, E6203"
/db xref="taxon:4081"
/clone="crOS17020"
/tissue type="muspension cultures"
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/lab_host="SOLR"
/lone lib="crOS"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
Xhol; Suspension cultures of i.esculentum E6203 were grown in Wurashige and Skoog based medium, supplemented with 15$ coconut milk (filter sterilized and added after autoclaving), 2$ saccharose, and lmg/ml 2,4D (pH5.8).
Fresh medium was added every 7 days, and cultures were grown at 25 C, with 12hrs of light and continuous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||||:::|||||| :::
CTTTCAACAAATTCTGAATTCAATTACCAGAAATTCGCATCTGTATTAGGTGTCAATCCA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 HisHisPheArgAlaValValGluAsnTyrIleThrAlaValLysAsnMetCysTyrAla 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ValleuGluLeuMetAlaGluGlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeu 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuLysAspGluLysSerAspSerCysPheArgLeuAsnHisTyrProProCysProGlu 190
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Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
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Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 776)
1 (bases 1, Watanabe, M., Yano, K., Suzuki, H., Sakurai, N. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||:::|||||||||||||||||::
TTGATTGGATTTGGAGAACATACTGACCCACAAATCATAGATCGATATAAGATCCAATAAC 637
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/clone="FC26CQ12"
/tisuc type="fruit"
/clone_lib="Lycopersicon esculentum cv. Micro-Tom fruit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ThrserPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPhe 256
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/mol_type="mRNA"
/cultivar="Micro-Tom"
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Location/Qualifiers
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BW692820.1 GI:62935234
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Matches:
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Mismatches:
Indels:
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December 28, 2005, 01:23:14; Search time 249 Seconds (without alignments) 2362.943 Million cell updates/sec
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                             - nucleic search, using frame_plus_p2n model
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BLOSUM62 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext Scoring table:

Title: Perfect score: Sequence:

OM protein

Run on:

1303057 segs, 888780828 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 1, Appli	Sequence 62, Appl	Sequence 7, Appli	Sequence 13, Appl	Sequence 5, Appli	Sequence 64, Appl	Sequence 3, Appli	Sequence 7, Appli	Sequence 1, Appli
SUMMAKIES	US-09-719-108-1	US-09-371-307-62	US-09-719-108-7	US-09-614-912-13	US-09-614-912-5	US-09-371-307-64	US-09-614-912-3	US-09-614-912-7	US-09-614-912-1
DB	m	m	٣	m	٣	m	m	m	m
% Query Match Length DB	1318	1359	1237	1352	1365	1403	1650	1473	1555
% Query Match	100.0	87.6	62.5	61.1	60.7	9.09	55.7	55.6	54.8
Score	1748	1530.5	1092.5	1068.5	1060.5	1060	973	972	957.5
Result No.	Ī	7	9	4	3	9	7	80	6

Appli	Appli	Appl	Appl	Appl	Appl	Appl	Appl	Appli	Appli	Appli	Appli	Appli	Appli	Appl	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appl	Appl	Appli	Appli	Appli	Appli	Appli	Appl	Appl	Appl	Appl	Appli
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9-719-108	09-719-108-	19-371-307	39-371-	US-09-371-307-71	US-09-371-307-68	-09-371-	US-09-371-307-66	-08-823-	US-08-784-385-1	PCT-US95-10403-1	US-08-379-556A-9	US-09-371-307-5	US-09-454-034-7	US-09-371-307-70	US-08-823-986A-3	US-08-784-385-3	US-08-379-556A-1	PCT-US95-10403-3	US-08-379-556A-7	US-08-553-367A-5	US-09-295-306-5	US-09-734-719-5	US-08-793-666-2	US-08-793-666-12	US-08-793-666-13	US-08-553-367A-3	ç	õ	-08-75	-08-55	-08-485-1	-08-793	-09-614-912	-09-371-3	US-08-553-367A-1
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ALIGNMENTS

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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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APPLICANT: Thomas, Stephen G
APPLICANT: Theden, Peter
APPLICANT: Hedden, Peter
APPLICANT: Hedden, Peter
TITLE OF INVENTION: Gibberellin 2-Oxidase
FILE REFERENCE: 0623.097000
CURRENT APPLICATION UNMBER: US/09/719,108
CURRENT APPLICATION NUMBER: PCT/GB99/01857
PRIOR PILING DATE: 1999-06-11
PRIOR PILING DATE: 1998-06-12
PRIOR PILING DATE: 1998-06-12
PRIOR PILING DATE: 1998-07-15
PRIOR PILING DATE: 1998-07-15
SROID NOS: 16
SOFTWARE: PATENTING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTING DATE: 1998-07-15
RESULT 1
US-09-719-108-1
; Sequence 1, Application US/09719108
; Patent No. 6670527
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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Application US/09371307A
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TYPE: DNA
CRGANISM: Glycine max
US-09-371-307-62
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Best Local Similarity:
Query Match:
DB:
 Sequence 62, Applicat
Patent No. 6723897
GENERAL INFORMATION:
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                             MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLysSer
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Patent No. 6677502
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Rafalski, Antoni
Orozco, Buddy
Miao, Gou-Hau
Famodu, Omolayo O.
Lee, Jian Ming
Sakai, Hajime
Weng, Zude
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                                                                                                                                                                                                                    TTTTCATCAATGTTGGTGACACTCTTCAGGTAATGACTAATGGGAGGTTTAAAAGTGTA
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                                                                                                          GlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProProAspGlnThrSer
                                                                                                                                                                                            PhePheileAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerVal
                        GlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsnSerThrSer
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APPLICANT: Thomas, Stephen G
APPLICANT: Hedden, Peter
APPLICANT: Hedden, Peter
TITLE OF INVENTION: Gibberellin 2-Oxidase;
FILE REFERENCE: 0623.097000
CURRENT APPLICATION NUMBER: US/09/719,108
CURRENT APPLICATION NUMBER: PCT/GB99/01857
PRIOR APPLICATION NUMBER: PCT/GB99/01857
PRIOR FILING DATE: 1999-06-11
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-07-15
NUMBER: OF SEQ ID NOS: 16
SEQ ID NO 7
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 7, Application US/09719108
; Patent No. 6670527
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; ORGANISM: Arabidopsis thaliana
US-09-719-108-7
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76.81%
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Best Local Similarity:
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       747 TTTGGAGAACACACAGACCCACAAATCATCTCTCTGTTAAGATCCAACAACAACTTCAGGC
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                                                                                PheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsnSerThrSerGly
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APPLICANT: Famodu, Omolayo O.

APPLICANT: Eee, Jian Ming
APPLICANT: Sakai, Hajime
APPLICANT: Meng, Zuda
APPLICANT: Caimi, Perry G
APPLICANT: Caimi, Perry G
APPLICANT: Caimi, Perry G
APPLICANT: Anderson, Shawn
TITLE OF INVENTION: Plant Metabolism Genes
FILE REFERENCE: BB1378 US NA
CURRENT APPLICATION NUMBER: US/09/614,912
CURRENT APPLICATION NUMBER: 60/143,401
PRIOR APPLICATION NUMBER: 60/143,401
PRIOR PILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/146,650
PRIOR PILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/146,650
PRIOR APPLICATION NUMBER: 60/170,906
PRIOR PILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: 60/172,959
PRIOR PILING DATE: 1999-12-21
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Matches:
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Patent No. 6677502
GENERAL INFORMATION
APPLICANT: Rafaleki, Antoni
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Rafalski, Antoni
Orozco, Buddy
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; ORGANISM: Glycine
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159 ATGGTGTTGTTGTCCAAAGAACAACAACAATACTCCTACATTAAGAACTGCATGCCA 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        399 AAGGAAAAAGTAGGACCTCCCAATCCATTTGGGTATGGTAGCAAGAAAATTGGACACAAT 458
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567 AIGTCTTCTGTGAGGAAGAATGGCATGAGATTCTTGAGTTGATGGCAGAAGGGTTGAAG 626
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Mismatches:
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APPLICANT: Caimi, Perry G
APPLICANT: Anderson, Shawn
TITLE OF INVENTION: Plant Metabolism Genes
FILE REFERENCE: BB1378 US NA.
CURRENT APPLICATION NUMBER: US/09/614,912
CURRENT APPLICATION NUMBER: 60/143,401
PRIOR PILING DATE: 1999-07-12
PRIOR FILING DATE: 1999-07-12
PRIOR FILING DATE: 1999-07-12
PRIOR FILING DATE: 1999-07-12
PRIOR FILING DATE: 1999-07-12
PRIOR PILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: 60/170,906
PRIOR APPLICATION NUMBER: 60/170,906
PRIOR FILING DATE: 1999-12-25
PRIOR APPLICATION NUMBER: 60/172,959
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/172,959
PRIOR FILING DATE: 1999-12-21
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77.95%
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SOFTWARE: Microsoft C
SEQ ID NO 13
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                                                                                                                                    APPLICANT: Brown, Sherri M.
APPLICANT: Brown, Sherri M.
APPLICANT: Heck, Gregory R.
APPLICANT: Heck, Gregory R.
APPLICANT: Bilch, Tedd D.
APPLICANT: Loguesch, Eugene W.
APPLICANT: Rach, Sudabathula
APPLICANT: Ream, Joel E.
APPLICANT: Ream, Joel E
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Matches:
Conservative:
Mismatches:
Indels:
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  1111 AATAGACTTGAACATTTTGAAAGAATTGCAGCT
                                                            US-09-371-307-64
; Sequence 64, Application US/09371307A
; Patent No. 6723897
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1060.00
76.44%
60.42%
60.64%
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Best Local Similarity:
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TITLE OF INVENTION: Plant Metabolism Genes
FILE REFERENCE: BB1378 US MS
FILE REFERENCE: BB1378 US MS
CURRENT APPLICATION NUMBER: US/09/614,912
CURRENT FILING DATE: 2000-07-12
PRIOR PILING DATE: 1999-07-12
PRIOR PILING DATE: 1999-07-12
PRIOR PILING DATE: 1999-07-12
PRIOR PILING DATE: 1999-07-30
PRIOR PILING DATE: 1999-07-30
PRIOR PILING DATE: 1999-07-30
PRIOR PILING DATE: 1999-12-15
PRIOR PILING DATE: 1999-12-21
PRIOR PILING DATE: 1999-12-21
SPRIOR PILING DATE: 1999-12-21
SOFTWARE: Microsoft Office 97
SOFTWARE: Microsoft Office 97
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Patent No. 6677502
GENERAL INFORMATION:
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Rafalski, Antoni
Orozco, Buddy
Miao, Gou-Hau
Famodu, Omolayo O.
Lee, Jian Ming
Sakai, Hajime
Weng, Zude
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ORGANISM: Oryza
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APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Grozco, Buddy
APPLICANT: Famodu, Cmolayo O.
APPLICANT: Famodu, Cmolayo O.
APPLICANT: Sakai, Hajime
APPLICANT: Weng, Zude
APPLICANT: Weng, Zude
APPLICANT: Weng, Shawn
TITLE OF INVENTION: Plant Metabolism Genes
FILE REFERENCE: BB1378 US /09/614,912
CURRENT APPLICATION NUMBER: US/09/614,912
CURRENT FILING DATE: 1999-07-12
PRIOR FILING DATE: 1999-07-12
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/143,412
PRIOR APPLICATION NUMBER: 60/143,412
PRIOR PLING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/146,650
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Patent No. 6677502
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Mismatches:
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                                                                                                                                                                                    APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Orozco, Buddy
APPLICANT: Orozco, Buddy
APPLICANT: Famodu, Omolayo O.
APPLICANT: Famodu, Omolayo O.
APPLICANT: Ee, Jian Ming
APPLICANT: Caimi, Perry G
APPLICANT: Caimi, Perry G
APPLICANT: Caimi, Perry G
APPLICANT: Anderson, Shawn
TITLE OF INVENTION: Plant Metabolism Genes
FILE REFERENCE: BB1378 US NA
CURRENT APPLICATION NUMBER: 06/143,401
PRIOR APPLICATION NUMBER: 60/143,412
PRIOR PILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/143,412
PRIOR PILING DATE: 1999-07-12
PRIOR PILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
PRIOR PILING DATE: 1999-12-15
PRIOR PRILCATION NUMBER: 60/170,906
PRIOR FILING DATE: 1999-12-11
PRIOR PILING DATE: 1999-12-21
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Patent No. 6677502
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Rafalski, Antoni
Orozco, Buddy
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; ORGANISM: Triticum aestivum
US-09-614-912-7
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Best Local Similarity:
Query Match:
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                                                               934 TTCATCTACTTCGCGGGGCCGCTGCGGGCAGCGGATCGCGCCGCTGCCGCAGTGCTG
                                                                                                                                                                       294 LeuLysGlyGluGluCysLeuTyrLysGluPheThrTrpCysGluTyrLysLysAlaAla
                                                 GlyargPheLysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSer
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                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMAS, Stephen G
APPLICANT: Thomas, Stephen G
APPLICANT: Hedden, Peter
TITLE OF INVENTION: Gibberellin 2-Oxidase
FILE REFERENCE: 0623.097000
CURRENT APPLICATION NUMBER: US/09/719,108
CURRENT APPLICATION NUMBER: US/09/719,108
CURRENT FILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: GB 9812821.8
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: GB 9812404.0
PRIOR FILING DATE: 1998-07-15
NUMBER: OF SEQ ID NOS: 16
SEQ ID NO 9
LENGTARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 1008
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US-09-719-108-9
; Sequence 9, Application US/09719108
; Patent No. 6670527
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; ORGANISM: Arabidopsis thaliana
US-09-719-108-9
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953.00
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Best Local Similarity:
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Pred. No.:
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Matches:
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PRIOR APPLICATION NUMBER: 60/1/0,200
PRIOR FILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: 60/172,959
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 204
SOFTWARE: Microsoft Office 97
SEQ ID NO 1
FUNCTH: 1555
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957.50
70.75%
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Best Local Similarity:
                                                                                                                                                         TYPE: DNA
ORGANISM: Zea mays
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Pred. No.:
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) ORGANISM: Arabidopsis thaliana

; FEATURE:

; NAME/KSY: misc feature

; LOCATION: (1243, 1265)

; OTHER INFORMATION: unidentified

US-09-719-108-5
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936.50
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Best Local Similarity:
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| AAAACCACCGCCATTTTCCGGCACACCCCTGCAATTTTCAGAGAGGCAGTGGAAGAGTAC
                                                                                                          ArgleuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly
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                                                          LysSerLeuCysllePheArgGluAsnProHisHisPheArgAlaValValGluAsnTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/09719108
; Sequence 5, Application US/09719108
; Patent No. 6670527
; GENERAL INFORMATION:
   APPLICANT: Thomas, Stephen G
   APPLICANT: Thomas, Stephen G
   APPLICANT: Phillips, Andrew L
   TITLE OF INVENTION: Gibberellin 2-Oxidase
   FILE REFERENCE: 06.23.0970000
CURRENT APPLICATION NUMBER: US/09/719,108
CURRENT PILING DATE: 2000-12-08
   PRIOR APPLICATION NUMBER: PCT/GB99/01857
   PRIOR FILING DATE: 1999-06-11
   PRIOR PILING DATE: 1999-06-12
   PRIOR FILING DATE: 1998-06-12
   PRIOR FILING DATE: 1998-06-12
   PRIOR FILING DATE: 1998-07-15
   NUMBER OF SEQ ID NOS: 16
   SOFTWARE: PatentIN Ver. 2.1
   SEQ ID NO 5
   LENGTHARE: PatentIN Ver. 2.1
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182 GGGCTAGGGATCAAACCGAGGAACACACTTAGCAAGCTTGTGTCTGACCAAAAACGGAC
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                                                                                                                                                                                                                                                                   349 TCTCTAAGAGAAGGAAGGAGTTTCAGTGCCACCTGACCAAACTCTCATTCTTCATTATT
                                                                                                                                  244 ValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLysHisArgVal
                                               224 CysieuThrAspGlyThrTrpValSerValProProAspGlnThrSerPhePhelleAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 58, Application US/09371307A
; Sequence 58, Application US/09371307A
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Piller, Kenneth J.
; APPLICANT: Elich, Tedd D.
; APPLICANT: Loguench, Eugene W.
; APPLICANT: Loguench, Eugene W.
; APPLICANT: Loguench, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Ream, Joel E.
; APPLICANT: Reprincible Methods for controlling gibberellin levels
; PILE REFERENCE: MOBT:216
; CURRENT APPLICANT: 1999-08-10
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE PATENTING DATE: 1999-08-10
; SOFTWARE PATENTING UNIVER: 2.0
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; ORGANISM: Arabidopsis thaliana
US-09-371-307-58
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Pred. No.:
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LENGTH: 966
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 275 ileTyrPheGlyGlyProAlaLeuSerGluAsnIjeAlaProLeuProSerValMetLeu 294
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                                                                                                                                                                                                                                                                            APPLICANT: Brown, Sherri M.
APPLICANT: Brown, Sherri M.
APPLICANT: Filter, Kenneth J.
APPLICANT: Filter, Kenneth J.
APPLICANT: Elich, Tedd D.
APPLICANT: Elich, Tedd D.
APPLICANT: Rao, Sudabathula
APPLICANT: Rogusch, Sherry J.
TITLE OF INVENTION: Methods for controlling gibberellin levels
FILE REFERENCE: MOST: 1999-08-10
CURRENT APPLICATION NUMBER: US/09/371,307A
CURRENT APPLICATION NUMBER: US/0871371,307A
CURRENT PILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin Ver. 2.0
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ORGANISM: Gossypium hirsutum
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OTHER INFORMATION:
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Best Local Similarity:
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LOCATION: (726)
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                             124 CysllePheArgGluAsnProHisHisPheArgAlaValValGluAsnTyrlleThrAla
                                                                                                                                                                      164 ArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPheArgLeuAsn
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Facent No. 6723897

GENERAL INFORMATION:

APPLICANT: Brown, Sherri M.

APPLICANT: Heck, Gregory R.

APPLICANT: Filer, Tedd D.

APPLICANT: Elich, Tedd D.

APPLICANT: Block, Ganesh M.

APPLICANT: Block, Ganesh M.

APPLICANT: Block, Ganesh M.

APPLICANT: Block, Ganesh M.

APPLICANT: Block, Mayene W.

APPLICANT: Ream, Joel E.

APPLICANT: Ream, Joel E.

TITLE OF INVENTION: Methods for controlling gibberellin levels

FILE REFERENCE: NOBT:216

CURRENT APPLICATION NUMBER: US/09/371,307A

CURRENT FILING DATE: 1999-08-10
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APPLICANT: Heck, Gregory R.
APPLICANT: Piller, Kenneth J.
APPLICANT: Filler, Kenneth J.
APPLICANT: Fishore, Ganesh M.
APPLICANT: Logusch, Eugene W.
APPLICANT: Rao, Sudabathula
APPLICANT: Rao, Sudabathula
APPLICANT: Logusch, Shorry J.
APPLICANT: Logusch, Shorry J.
TITLE OF INVENTION: Methods for controlling gibberellin levels
FILE REFERENCE: MOBT:216
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Mismatches:
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Matches:
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Patent No. 6723897
GENERAL INFORMATION:
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; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 71
; LENGTH: 811
; TYPE: DNA
; ORGANISM: Zea mays
US-09-371-307-71
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Query Match:
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61

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183 AsnHisTyrProProCysProGlu---ValGlnAlaLeuAsn------ArgAsnLeu 198
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                                                                                                                                                                                                                                                                                                                                                                             143 AlayaliysAsnMetCysTyrAlaValieuGluLeuMetAlaGluGlyLeuGlyIleArg 162
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CURRENT APPLICATION NUMBER: US/09/371,307A CURRENT FILING DATE: 1999-08-10 NUMBER OF SEQ ID NOS: 89 SEQ TWARE: Patentin Ver. 2.0 SEQ ID NO 68 LENGTH: 406
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67, Appl 1, Appl 1, Appl 1, 608, A 12930, A 12930, Appl 58, Appl 2, Appl 159585, A

71, Appl 71, Appl 614, App 9278, Ap 82069, A 68, Appl 68, Appl 57, Appl

Title: Perfect score:

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US-10-821-711-3
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Best Local Similarity:
Query Match:
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Alignment Scores:
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Sequence 7, Appli
                                                                                                                December 28, 2005, 01:30:23 ; Search time 975 Seconds (without alignments) 2807.348 Million cell updates/sec
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-401-321-62
US-09-938-842A-1350
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                 Met Val Val Leu Ser Gln Pro Ala Leu Asn Gln Phe Phe Leu Leu Lys Pro Phe Lys Ser
                            ATGGTTCTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAAACCATTCAAGTCC
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US-10-670-454-2 (1-331) x US-10-821-711-3 (1-999)
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81 LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly 41 IleValAsnAlaCysArgAspPheGlyPheDysLysLeuValAsnHisGlyValProLeu 188 ATAGTGAACGCCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCCATTG 308 AAAGACAGAGCTGGTCCCCCCGGACCCTTTCGGCTATGGTAGCAAGAGGATTGGCCCAAAC | IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 1318 331 0 0 0 Length: Matches: Conservative: Mismatches: US-10-670-454-2 (1-331) x US-10-670-454-1 (1-1318) GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Thomas, Stephen G
APPLICANT: Thomas, Stephen G
APPLICANT: Hedden, Peter
APPLICANT: Hedden, Peter
APPLICANT: Hedden, Peter
APPLICANT: Hillips, Andrew L
TITLE OF INVENTION: Gibberellin 2-Oxidase
FILE REFERENCE: 0623.0970000
CURRENT APPLICATION NUMBER: US/09/719,108
PRIOR PRILING DATE: 2003-09-26
PRIOR PRILING DATE: 2000-12-08
PRIOR PRILING DATE: 1999-06-11
PRIOR PLILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: PCT/GB99/01857
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-07-15
SPOID NOS: 16
SOFTWARE: PATENTIN VET: 2.1 Indels: 3.55e-219 1748.00 100.00\$ 100.00\$ coccineus TYPE: DNA ORGANISM: Phaseolus Percent Similarity: Best Local Similarity: Query Match: DB: 181

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            GluleuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu
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US-10-401-321-62
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TTTGGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTAACAGCACACTCTGGC
                                                                                                                                                                                          TTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTGTAAAG
                                  PheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsnSerThrSerGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 62, Application US/09371307A

Sequence 62, Application US/09371307A

Patent No. US20020053095A1

GENERAL INFORMATION:

APPLICANT: Broam, Sherri M.

APPLICANT: Piller, Kenneth J.

APPLICANT: Fishore, Gamesh M.

APPLICANT: Elich, Tedd D.

APPLICANT: Logusch, Eugene W.

APPLICANT: Rao, Sudabathula

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Matches:
Conservative:
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1530.50
90.36%
89.16%
87.56%
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; ORGANISM: Glycine max
US-09-371-307-62
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LENGTH: 1359
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US-09-371-307-62
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Harper, Joef
APPLICANT: Wang, Xun
APPLICANT: SANG, AND METHODS OF USE
TITLE OF INVENTION: STAE, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT APPLICATION NUMBER: US 60/227,866
PRIOR PELING DATE: 2000-08-24
PRIOR PELING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-06-22
NUMBER OF SEQ ID NOS: 5379
LENGTH: 1026
                                                                                                                          ProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCys 299
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                        882 AAGCATAGAGTTTTGGCTGACCCAAGTCAAGGTTGTCAATGATCTACTTTGGAGGA
                                                                                                                                           942 CCACCCTTGTGTGAAAAGATAGCACCTTTACCTTCACTCATGTTAAAAGGAGAAGAGAGT
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                                                                 LysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGly
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1062 GATAATAGACTCGGCCCTTTTGAGAAATCTGCTGCT 1097
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                               ; Sequence 1350, Application US/09938842A ; Patent No. US20020160378A1
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1092.50
76.81%
63.25%
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Query Match:
DB:
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US-09-938-842A-1350
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Percent Similarity:
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APPLICANT: Ream, Joel E.
APPLICANT: Logusch, Sherry J.
APPLICANT: Logusch, Sherry J.
APPLICANT: Baerson, Scott R.
TITLE OF INVENTION: Methods for Controlling Gibberellin Levels
FILE REFERENCE: 11899.0216.DVUS01 (MOBT:216--1)
CURRENT APPLICATION NUMBER: US/10/401,321
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.2
ENGTH: 1359
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Matches:
Conservative:
Mismatches:
Indels:
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1530.50
90.36%
89.16%
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                    TYPE: DNA
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Matches:
Conservative:
Mismatches:
Indels:
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                   ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1350
                                                                         6.49e-133
1092.50
76.81%
63.25%
62.50%
                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
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SEQ ID NO 1350
LENGTH: 1026
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           CCTCAGTCTCTTAAAAACCGGGCCGGTCCACCTGAACCGTACGGTTATGGTAATAAACGG
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US-09-938-842A-1350

Squence 1350, Application US/09938842A

Publication No. US20040009476A9

GENERAL INFORMATION:
APPLICANT: Harper, Jeff

APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: About Tong
TITLE OF INVENTION: SAME, AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/224,647

PRIOR PILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

HORDER OF FILING DATE: 2001-01-16

HORDER PLOATION NUMBER: US 60/300,111

HORDER OF SEQ ID NOS: 5379
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                      886 AAGAGTGTTAAACACAGGGTCTTAGCCGATACAAGGAGATCGAGGATTTCAATGATATAT
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APPLICANT: Brown, Sherri M.
APPLICANT: Brown, Sherri M.
APPLICANT: Biller, Kenneth J.
APPLICANT: Filler, Kenneth J.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Logusch, Fugene W.
APPLICANT: Rao, Sudabathula
APPLICANT: Rao, Sudabathula
APPLICANT: Logusch, Sherry J.
TITLE OF INVENTION: Methods for controlling gibberellin levels
FILE REFERENCE: MOBF:216
CURRENT APPLICATION NUMBER: US/09/371,307A
CURRENT FILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 64
LENGTH: 1403
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Matches:
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f ORGANISM: Glycine max
US-09-371-307-64
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                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
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US-10-670-454-7

US-10-670-454-7

Sequence 7, Application US/10670454

PUDLication No. US20040229357A1

GENERAL INFORMATION:

APPLICANT: Thomas, Stephen G

APPLICANT: Hedden, Peter

APPLICANT: Hedden, Peter

TITLE OF INVENTION: Gibberellin 2-Oxidase

FILE REFERENCE: 0623.0970000

CURRENT APPLICATION NUMBER: US/10/670,454

CURRENT FILING DATE: 2000-12-08

PRIOR FILING DATE: 2000-12-08

PRIOR FILING DATE: 1999-06-11

PRIOR FILING DATE: 1999-06-12

PRIOR FILING DATE: 1999-06-12

PRIOR FILING DATE: 1999-06-12

PRIOR FILING DATE: 1999-06-12

PRIOR FILING DATE: 1999-07-15

NUMBER OF SEQ ID NOS: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-670-454-7
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                                                                                         APPLICANT: Brown, Sherri M.
APPLICANT: Heck, Gregory R.
APPLICANT: Filler, Kenneth J.
APPLICANT: Filler, Kenneth J.
APPLICANT: Filler, Ganesh M.
APPLICANT: Rao, Gudabathnia
APPLICANT: Rao, Sudabathnia
APPLICANT: Rao, Joele W.
APPLICANT: Barenon, Scott R.
TITLE OF INVENTION: Methods for Controlling Gibberellin Levels
FILE REFERENCE: 11899 0216 DV1801 (MOBT:116-1)
CURRENT APPLICATION NUMBER: US/10/401,321
CURRENT APPLICATION NUMBER: US/10/401,321
CURRENT PAPLICATION NUMBER: 108/10/401,321
SOFTWARE: Patentin Version 3.2
SOFTWARE: Patentin Version 3.2
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                                                       ; Sequence 64, Application US/10401321; Publication No. US20030233679A1; GENERAL INFORMATION:
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: East Thomas J
APPLICANT: East Thomas J
APPLICANT: About Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENITION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENITION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 21951
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                                                                      PheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsnSerThrSerGly
                       ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly
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Sequence 78659, Application US/10437963
; Sequence 78659, Application US/20343341
; Publication No. US20040123343A1
; Publication No. US20040123343A1
; Replicant: Royalic, David K.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; APPLICANT: Bucharov, Andrey A.
; APPLICANT: Bucharov, Andrey A.
; APPLICANT: Bucharov, Andrey A.
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION UMBER: US/10/437,963
; CURRENT PILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 78659
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US-10-437-963-78659
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ORGANISM: Oryza sativa
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US-10-437-963-78659
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APPLICANT: Sakai, Miho
TITLE OF INVENTON: GIBBERELLIN 2-OXIDASE GEN
FILE REFERENCE: SHZ-014
CURRENT APPLICATION NUMBER: US/10/392,325
CURRENT FILING DATE: 2003-03-18
NUMBER OF SEQ ID NOS: 7
PRIOR PRICK APPLICATION NUMBER: US 2002-276051
PRIOR FILING DATE: 2002-09-20
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: (1)..(984)
OTHER INFORMATION:
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US-10-392-325-3
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Matches:
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                                     Clone ID: MRT4577_163444C.1
                                                                                         8.42e-115
957.50
70.75%
57.01%
54.78%
                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
            CRGANISM: Zea mays
FEATURE:
CTHER INFORMATION:
US-10-425-115-69575
                                                                              Alignment Scores:
Pred. No.:
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Squence 69575, Application US/10425115
GRNERAL INFORMATION:
GRNERAL INFORMATION:
GRNERAL INFORMATION:
APPLICANT: Land St.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Con Young K.
APPLICANT: Con Young K.
APPLICANT: Con Young K.
APPLICANT: Con Young K.
APPLICANT: Shou, Yihua
APPLICANT: Shou, Yihua
APPLICANT: Shou, Young K.
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SUMBER OF SEQ ID NOS: 369326
SEQ ID NO 69575
LENGTH: 1611
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60 LeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSer
               320 ACGGACACGATGGACAAAGGCCGAGAGGCCGTCAGGTTCTTCTTCTCCCAGACGCCC
                                                    GluLysAspargAlaGlyProProAspProPheGlyTyrGlySerLysArglleGlyPro
                                                                                                                     116 AspValIleSerProLysSerLeuCysIlePheArgGluAsnProHisHisPheArgAla
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   LysSerLeuCysIlePheArgGluAsnProHisHisPheArgAlaValValGluAsnTyr 140
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                                                                                                                                                181 ATAGAGCCAAAGGAGAAGCTGAGCCGTTTGGTGAAAGTGAAAGTGATTCGTGCCTG
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APPLICANT: Provart, Nicholas
APPLICANT: Ricke, Darrell
APPLICANT: Ricke, Darrell
APPLICANT: APLICANT: Tong
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
FILE REFERENCE: 70029-NP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT ACTION UTMBER: US/10/259,194A
CURRENT FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR APPLICATION NUMBER: US 60/370,743
PRIOR APPLICATION NUMBER: US 60/370,743
PRIOR FILING DATE: 2002-04-04
PRIOR FILING DATE: 2002-04-04
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 662
SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
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; Publication No. US20040010815A1
; GENERAL INFORMATION:
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Goff, Stephen A.
Katagiri, Fumiyaki
Kreps, Joel
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Briggs, Steven P.
Cooper, Bret
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US-10-259-194A-141
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181 GATCTTTTGACTCAGTTGGAGCAAGAAGCCATCAACTTCTTTGCTTTGCATCACTCTCTC 240
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                                             LeuLysGlyGluGluCysLeuTyrLysGluPheThrTrpCysGluTyrLysLysAlaAla
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                                                                                                                                                                                                                                   APPLICANT: Thomas, Stephen G
APPLICANT: Hedden, Peter
APPLICANT: Hedden, Peter
APPLICANT: Hedden, Peter
APPLICANT: Hedden, Peter
TILE OF INVENTION: Gibberellin 2-Oxidase
FILE REFERENCE: 0623.0970000
CURRENT APPLICATION NUMBER: US/09/719,108
PRIOR APPLICATION NUMBER: US/09/719,108
PRIOR APPLICATION NUMBER: ET/GB99/01857
PRIOR APPLICATION NUMBER: GB 9812821.8
PRIOR APPLICATION NUMBER: GB 9815404.0
                                                                                                                                                                                            ; Sequence 9, Application US/10670454; Publication No. US20040229357A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-670-454-9
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953.00
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SOFTWARE: PatentIn Ver. 2.1
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Query Match:
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US-10-670-454-9
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181 ACGGACACGATGGACAAGGCCGAGGCCGTCAGGTTCTTCTCCCAGACGCAGCCC 240
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                                                                                                                                             60 LeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSer 79
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                                                              927
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                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                              2.93e-114
950.50
71.21%
56.36%
54.38%
                 TYPE: DNA
ORGANISM: Oryza sativa
                                                                               Percent Similarity:
Best Local Similarity:
                           ; ORGANISM: Oryz;
US-10-259-194A-141
                                                    Alignment Scores:
SEQ ID NO 141
LENGTH: 927
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27, Appl 13513, A 8, Appli

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Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

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Sequence 13513, A Sequence 3436, A Appli Sequence 13426, A Sequence 13426, A Sequence 13436, A Sequence 13, Appli Sequence 51, Appli Sequence 51, Appli Sequence 211, Appli Sequence 211, Appli Sequence 1129, Appli Sequence 1129, Appli Sequence 1129, Appli Sequence 1129, Appli Sequence 117, Appli Sequence 17, Appli Sequence 11384, A Sequence 13431, A Sequence 13431, A Sequence 13843, A Sequence 13843, A
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Sequence 5, Appli
Sequence 77, Appli
Sequence 77, Appl
Sequence 92, Appl
Sequence 590, Appl
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APPLICANT: Schomburg, Fritz M.
APPLICANT: Midaels, Scott D.
APPLICANT: Midaels, Scott D.
APPLICANT: Midaels, Scott D.
APPLICANT: Midaels, Scott D.
TITLE OF INVENTION: Dwarfism Genes and Dwarf Plants
FILE REFERENCE: 960296.97605
CURRENT APPLICATION NUMBER: US/11/152,892
CURRENT APPLICATION NUMBER: US/10/155,435
PRIOR APPLICATION NUMBER: US/2002-05-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NOS: 12
SEQ ID NOS: 12
SEQ ID NOS: 12
7 US-11-055-309A-2
7 US-11-034-771-1
7 US-11-121-066-77
6 US-10-995-561-13513
6 US-10-995-561-13294
6 US-10-995-561-13294
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9 US-11-082-389-51
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Matches:
Conservative:
Mismatches:
Indels:
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Publication No. US20050251883A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.46e-29
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Pred. No.:
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-LOOPCL=0 -LOOPEXT=0 -UNITS=b1ts -START=1 -END=-1 -MATRIX=b1osum62
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 3, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 82, Appli
Sequence 50357, A
Sequence 14, Appl
                                                                                                                                                                                                         December 28, 2005, 01:42:45; Search time 786 Seconds (without alignments) 220.763 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/USO8 NEW PUB.seq:*

2: /cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*

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5: /cgn2_6/ptodata/1/pubpna/USO7_NEW PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/USO1_NEW PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/USO1_NEW PUB.seq:*

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8: /cgn2_6/ptodata/1/pubpna/USO1_NEW PUB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USO1_NEW PUB.seq:*

10: /cgn2_6/ptodata/1/pubpna/USO1_NEW PUB.seq:*
                                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                                                                                          OM protein - nucleic search, using frame plus p2n model
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US-11-152-892-3
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US-11-152-892-1
US-11-058-817A-3
US-11-121-066-82
US-10-517-605-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4172979 seqs, 262114271 residues
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Maximum Match 100%
Listing first 45 summaries
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Kgapop 10.0 , Kgapext 0
Kgapop 10.0 , Kgapext C
Fgapop 6.0 , Fgapext 7
Delop 6.0 , Delext 7
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Maximum DB seq length: 200000000
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Match Length DB
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Database :

Score

Result

325.5 288 173 169.5 89.5 83.5 82.5

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APPLICANT: Amasino, Richard M.
                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                SEQ ID NO 3
LENGTH: 1011
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                                                      GlySerLysArglleGlyProAsnGlyAspValGlyTrpValGluTyrLeuLeu---- 110
                                                                                                                                                                                                                                   -----LeuAsnThrAsnProAspValIleSerProLysSerLeuCysIlePheArg 127
                                                                                                                                                                                                                                                                                                          128 GluAsnProHisHisPheArgAlaValValGluAsnTyrIleThrAlaValLysAsnMet 147
                                                                                                                                                                                                                                                                                                                           460 --------ACAATGGAGAAATTTGCTTCGGAATCAGAGCATTA 495
                                                                                                                                                                                                                                                                                                                                                   148 CysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGlyIleArgGlnArgAsnThrLeu 167
                                                                                                                                                                                                                                                                                                                                                                                              SerArgLeuLeuLysAspGlu---LysSerAspSerCysPhe---ArgLeuAsnHisTyr 185
                                                                                                                                                                                                                                                                                                                                                                                                            ProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGlyPheGlyGluHisThr 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 AspProGlnIlelleSerValLeuArgSerAsnSerThrSerGlyLeuGlnIleCysLeu 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226 ThrAspGlyThrTrpValSerValProProAspGlnThrSerPhePheIleAsnValGly 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 AspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLysHisArgValLeuAla 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      266 AspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyProAlaLeuSerGluAsn 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     886 ATA-----GAGTGTTCAAGTGTCCTGCT 912
                                                                                                                                                                         75 -----LysLysSerGlnSerGluLysAspArgAlaGlyProProAspProPheGlyTyr 92
                                                                                                                                74
                                          58 ValProLeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePhe-----
                                                                                                                                                                                                                                                                                                                                                                 38 LysAsnLeulleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGly
                                                                                                                                                                                                                                                                                    415 ATGACAGATATTTCTGACAACAACACTTTACTACTCTCAGCTCA----
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12
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                    US-10-670-454-2 (1-331) x US-11-152-892-5 (1-1017)
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Publication No. US20050251883A1
GENERAL INFORMATION:
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US-11-152-892-3
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370 ACTICTCCCGCTCAGTACTCCGTTTCGGAAGCGTTTCACATCATTCTTCAGAGGTTTCA 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGAAACAAATGGTTGCAGCTGCGAAAGAGTGGGGGATTTTTTCAAATTGTGAACCATGGA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlyProAsnGlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspVal 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 GGA-----AACCCTAGGCC 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 ---PheArgGluAsnProHisHisPheArgAlaValValGluAsnTyrIleThrAlaVal 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 LysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGlyIleArgGlnArg 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AsnThrLeuSerArgLeuLeuLysAsp-----GluLysSerAspSerCysPheArgLeu 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    535 AACGTGAGTTCGGAGTATTTCGAAACATTTTTGAGCTTGAAAACAGTTTTCTAAGGCTC 594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 TTTTCTGTGAAAGTCAGAGAAAGTTTTTCGGAC---TTATCGAAGAATAGTTACCGTTGG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 ValProLeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPheLysLysSer 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlnSerGluLysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIle 97
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79
59
110
66
APPLICANT: Schomburg, Fritz M.
APPLICANT: Bizzli, Colleen M.
APPLICANT: Bizzli, Colleen M.
TITLE OF INVENTION: Dwarfism Genes and Dwarf Plants
FILE REFERENCE: 960.296.97605
CURRENT APPLICATION NUMBER: US/11/152,892
CURRENT FILING DATE: 2005-06-15
PRIOR APPLICATION NUMBER: US/10/155,435
PRIOR APPLICATION NUMBER: US/10/155,435
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
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Matches:
Conservative:
Mismatches:
Indels:
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288.00
43.95%
25.16%
                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: CDS
; LOCATION: (1)..(1008)
US-11-152-892-3
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Best Local Similarity:
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Db 643 CCTCATACCGATACAAGTTTTCTCACTATACTCTCTCAAGATCAAATCGGAGGGTTAGAA 702	Db 3279 TIGTATCAAGATCAAGTCGGAGGACTCCAACTTATCAAAGACAATAGATGGATCGCT 3335
Qy 223 IleCysLeuThrAspGlyThrTrpValSerValProProAspGlnThrSerPhePheIle 242	Qy 233 ValProProAmpGlnThrSerPhePheIleAmValGlyAmpAlaLeuGlnVal 250
Db 703 TTGGAAAATAATGGACAATGGATCAGCGTAAAACCTTGGTAGGAAGCCCTTACAGTC 759	Db 3336 GTTAAACCTAAAGCTCTCATTATCAATATTGGTGACTTATTCAGGTAATTGAG 3395
Oy 243 AsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLysHisArg 262	Qy 250 250
Db 760 AACATTGGGGATATGTTTCAGGCACTGAGTAATGGAGTGTACCAAAGCGTGAGACATAGA 819	Db 3396 CTTTTATTATGTCATTCTACCATTACCATTATATCGGGAGCTTACAAATTAGTT 3455
Oy 263 ValbeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyGlyFroAlaLeu 282	Qy 250 250
Db 820 GTGATTCTCCAGCAAATATCGAGAGGATGTCAATAGCTTTCTTCGTATGTCTTATCTC 879	Db 3456 TGGTATTTTATGTTTTGATATGGTTTTGGAAGGATTTAAACAATTTGTTCATACGCATGCA 3515
Oy 283 SerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCysLeu 300	Qy 250 250
Db 880 GAAACTGAGATC06	Db 3516 TGATCAATAAAAATTAAAAATGGGATTTCTTATAAAGGTAACATCTAAGGCAATGTATTAAA 3575
Qy 301TyrLysGluPheThrTrpCysGluTyrLysLys 311	Qy 251
Db 907 CCAAAGAAGTATAGAAGATTCAGTTTCAGAGAGTACAAAGAG 948	Db 3576 AATGTCTTTAAATTACTAGATTGTACTTATATATGTGTTTGGTTAGGCATGGAGCAATGG 3635
RESULT 3 US-11-152-892-2 ; Sequence 2, Application US/11152892	Oy 254 yArgPheLysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMe 274
	Qy 274 tlleTyrPheGlyGlyProAlaLeuSerGluAsnileAlaProLeuProSerValMetLe 294
<pre>; APPLICANT: Amasino, Richard M. ; APPLICANT: Schomburg, Fritz M.</pre>	Db 3696 GGCTTATTTATGTGTCCATCATACGACGCCGTTATA3732
; APPLICANT: Michaels, Scott D. ; APPLICANT: Bizzell, Colleen M. : TITLE OF INVENTION: Dwarfism Genes and Dwarf Plants	Qy 294 uLy8GlyGluGluCy8LeuTyrLy8GluPheThrTrpCy8GluTy 309
FILE REFERENCE: 960296.97605	Db 3733GAGTGTTCAAGTGATCGTCCTGCTTATAGAAATTTCAGCTTCAGAGAATT 3782
CURRENT FILING DATE: 2005-06-15 PRIOR APPLICATION NUMBER: US/10/155, 435	Qy 309 rLysLys 311
PRIOR FILING DATE: 2002-05-23 NIMBER OF SEC ID NOS: 12	Db 3783 CAGACAA 3789
လ	RESULT 4 US-11-152-892-1
LENGTH: 3861 TYPE: DNA	; Sequence 1, Application US/11152892 ; Publication No. US20050251883A1
; ORCANISM: Arabidopsis US-11-152-892-2	; GENERAL INFORMATION: ; APPLICANT: Amesino, Richard M.
cores:	; APPLICANT: Schomburg, Fritz M.
9.08e-10 173.00 36.12%	; APPLICANT: Bizzell, Colleen M.; ; TITLE OF INVENTION: Dwarfism Genes and Dwarf Plants; FILE REFERENCE: 960296.9760
Mismatches: Indels: Gans:	; CURRENT APPLICATION NUMBER: US/11/152,892 ; CURRENT FILING DATE: 2005-06-15 ; PRIOR APPLICATION NUMBER: US/10/155.435
10-670-454-2 (1-331) x US-11-152-892-2 (1-3861)	PRIOR FILING DATE: 2002-05-23
aValValGluAвnTyrIleThrAlaValLysAвлМеtСуяТүrAlaValLeu	; SOFTWARE: Patentin Ver. 2.1 ; SEQ ID NO 1
bb 3066 TCAACAATGGAGAAATTTGCTTCGGAATCAGAGGCATTAGCATAGTATGTTGGCAGAGGTT 3125	TYPE: DNA
talagluGlyLeuglyIleArgGlnA	; OKGANISM: ATABIGODBIB US-11-152-892-1
Db 3126 CTTGCAGAAAATCTGGACAAAATTCAAGTTTCTTCAAAGAAAAC 3170	Length
Qy 175LysSerAspSerCysPheArgLeuAsnHisTyrProProCysProGluValGln 192	Score: 169.50 Matches: 74 Percent Similarity: 30.84% Conservative: 54 Rest Local Similarity: 17.83% Mismatches: 96
193 AlaLeuAsnAroAsnLeuValGlvPheGlvGluHisThrAsnProGlnIleIleSerVal	9.70% Indels:
3231GAGGTGTACGGATTAATGCCACACGGACAGTGATTTCCTCACAATC	-10-670-454-2 (1-331) x US-11-152-892-1 (1-2171)
Oy 213 LeuargSerAsnSerThrSerGlyLeuGln1leCysLeuThrAspGlyThrTrpValSer 232	Cy 27 IleProValValAspLeuThrHisProAspAlaLys 38
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230 TrpValSerValProProAspGlnThrSerPhePheIleAsnValGlyAspAlaLeuGln 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              880 TTGCTCACACCATTTGCTGAAATACCATTCATGGCTGTTTTTCCAGCTTTTGGTTTC--- 824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 LysLeuValAsnHisGlyValProLeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 AspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspVal---IleSerPro
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1288 GTAATTACTTCTACCCTTTGATTTTCAACGTTCAAGTCCATTAAG 1332
                                                                                                                         250 ValMetThrAsn-----GlyArgPheLysSerValLys 260
                                                                                                                                                                                                                                                             Sequence 3, Application US/11058817A
; Bublication No. US20050262580A1
; GENERAL INFORMATION:
; APPLICANT: Petrukhin, Konstatin
; APPLICANT: Petrukhin, Konstatin
; APPLICANT: Petrukhin, Konstatin
; APPLICANT: Petrukhin, Konstatin
; TITLE OF INVENTION: Transgenic Mouse with a targeted
; TITLE OF INVENTION: deletion of ELOVL4 Gene
; FILE REFERENCE: 21550
; CURRENT APPLICATION NUMBER: US/11/058,817A
; CURRENT APPLICATION NUMBER: 60/545,358
; PRIOR FILING DATE: 2004-02-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 967
; TYPE: DAM
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925 TTTTTCTGCTTTTTTCCATGAGTTGTTTTTCT
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Mismatches:
Indels:
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Matches:
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21.62
5.12$
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Best Local Similarity:
Query Match:
DB:
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ORGANISM: human
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                                                       68190 CTACTGCAACAGCTTCTTATCTATTTCTATTTTCAACTCTTGCCTTCCTCT-------
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                                 -----LysAsnMetCysTyr-AlaValLeuGluLeuMetAlaGluGlyLeuGlyIl
                                                                                                                                                                                                                                                  201 eGlyGluHisThrAspProGlnIleIleSerVal---LeuArgSerAsnSerThrSerGl
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APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: MAILLOO-2
CURRENT APPLICATION NUMBER: US/10/750,185
PRIOR APPLICATION NUMBER: US/0/437,482
PRIOR PILING DATE: 2003-12-31
PRIOR PILING DATE: 2002-12-31
NUMBER OF SEC ID NOS: 64922
SOFTWARE: PATENTIN version 3.1
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Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: RERR, Richard
APPLICANT: ROSENFELD, David
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Best Local Similarity:
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                                                                                                                                                                    LeuArgSerAsnSerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTrpValSer 232
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                                                                                                       541 recrechaeceaertraarrecaarecaeaaggraaacaregraeagreargaraaraaca 482
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Publication No. US20050266459A1
Publication No. US20050266459A1
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT PILING DATE: 2005-05-04
PRIOR FILING DATE: 2004-05-04
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                                   574 GGAATTCAACTGGGCTCCAAAAAATGCTTGTCC
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SOFTWARE: Patentin version 3.3
SEQ ID NO 82
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US-11-121-086-82
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Qy 130 ProhishisPheArgAlaValValGluAsn	Qy 197 AsnLeuValGlyPheGlyGluHisThr 205	Jight Human 190 Length: 5515
Qy 191 ValGlnAlaLeuAsnArgAsnLeuValGlyPheGlyGluHisThrAspProGlnIleIle 210 Db 824 GTTCAGGCT	Qy 266 AspThrThrLysSerArgLeuSerMetlleTyrPheGlyGlyProAlaLeuSerGluAsn 285	Alignment Scores:

Alignment Scores: 215 Length: 5982 Pred. No.: 215 Matches: 40 Score: 82.50 Matches: 40 Percent Similarity: 36.69\$ Conservative: 22 Best Local Similarity: 23.67\$ Mismatches: 64 Query Match: 77\$ Gaps: 7	US-10-670-454-2 (1-331) x US-11-034-771-1 (1-5982) Qy 75 LysLysSerGluLysAspArgAla	bb 5151 AGGAAATCACAGGGGGGGCCAGCAGGAGACGTGAAACTTGGTGAATCTTTATTAAACTAG Qy 85 GlyProProAspProPheGlyTyrGlySerLysArglle	5091		4.	Oy 130 ProHisHisPheArgAlaValValGluAsn	Qy 140TyrlleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGly	159 LeuGlylleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspG	Alzheimer's Oy 179 CysPheArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArg	Oy 197 ABILEUVAIGIYPHEGIYGIUHisThr 205	RESULT 11 US-11-121-086-27/c ; Sequence 27, Application US/11121086 ; Publication No. US20050266459A1	; GENERAL INFORMATION: ; APPLICANT: POULSEN, TIM S. ; APPLICANT: NIELSEN, KIRSTEN V. ; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES; FILE REFERENCE: 09138.6000-00000	CURRENT APPLICATION NUMBER: US/11/121,086 ; CURRENT FILING DATE: 2005-05-04 ; PRIOR APPLICATION NUMBER: 60/567,570 ; PRIOR FILING DATE: 2004-05-04	; NUMBER OF SEQ ID NOS: 107 ; SOTTWARE: PatentIn version 3.3 ; SEQ ID NO 27 ; LENGTH: 153142	; ITE: DNA ; ORGANISM: Homo sapiens US-11-121-086-27	Alignment Scores: 3.16e+04 Length: 153142 Pred. No.: 82.50 Matches: 40 Score: 9ercent Similarity: 36.69% Conservative: 22 Best Local Similarity: 23.67% Mismatches: 64
Oy 110 LeuLeuAsnThrAsnProAspValIleSerProLysSerLeuCysIlePheArgGluAsn 129	Oy 140TyrIleThralaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGly 158 :::	Qy 159 LeuGlylleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSer 178	CysPheArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArg	Oy 197 AsnLeuValGlyPheGlyGluHisThr 205	ESULT 10	US-11-034-//1-1/C ; Sequence 1, Application US/11034771 ; Publication No. US20050277129A1 ; GENERAL INFORMATION:	; APPLICANT: Aerssens, Jeroen ; APPLICANT: Athanasiou, Maria ; APPLICANT: Brain, Carlos ; APPLICANT: Cohen Nadine	Dain, Denton Judson Ozdem	; APPLICANT: Reed, Carol R. ; TITLE OF INVENTION: APOE Genetic Markers Associated with Age of Onset of Alzh ; TITLE OF INVENTION: Disease ; FILE REPERENCE: 2300.0130001	; CURRENT APPLICATION NUMBER: US/11/034,771 ; CURRENT FILIAG DATE: 2005-01-14 ; PRIOR APPLICATION NUMBER: US 60/538,590 ; PRIOR FILING DATE: 2004-01-22	; NUMBER OF SEO ID NOS: 42 ; SOFTWARE: Patentin version 3.3 ; SEO ID NO 1 ; LENGTH; 5982 ; TYPE: DNA	; ORGANISM: Homo sapiens ; FEATURE: ; NAME/KEY: misc_feature ; LOCATION: (1102)(1102) ; OTHER INFORMATION: n is 't' or 'c'	KE: KEY: misc feature ION: (1641)(1641) INFORMATION: n is 'c' or	: misc_feature : (2476)(2476) FORMATION: n is 'g' or	; FEATURE: ; NAME/KEY: misc feature ; LOCATION: (4415)(415) ; OTHER INFORMATION: n is 't' or 'c'	, o,

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Sequence 8, Application US/10501675

Publication No. US20050282161A1

GENERAL INFORMATION:

APPLICANT: TANABE SELYAKU CO., LTD.

TITLE OF INVENTION: A Novel Phospholipase A2 and the gene thereof.

TITLE OF INVENTION: A Novel Phospholipase A2 and the gene thereof.

CURRENT APPLICATION NUMBER: US/10/501,675

CURRENT APPLICATION NUMBER: US/00-167

PRIOR PILING DATE: 2004-07-16

PRIOR FILING DATE: 2002-01-17

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin Ver. 2.0

LENGTH: 3587
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US-10-501-675-8
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US-10-501-675-8
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; CTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13513
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|2920 AGGAAATCACAGGGGAGGCCAGCAGATGCGTGAAACTTGGTGAATCTTTATTAAACTAG 72861
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US-200-13513, Application US/10995561

Sequence 13513, Application US/10995561

PUBLICATION NO. USCOSO272054A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

TITLE OF INVENTION: DETECTION AND USES THEREOF

TITLE OF INVENTION: DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FRAESEQ for Mindows Version 4.0
                                                                                                                                                                                                            GlyProAsnGlyAspValGlyTrp--------ValGluTyrLeu 109
                                                                                                                                                                                                                                                                              110 LeuLeuAsnThrAsnProAspValIleSerProLysSerLeuCysIlePheArgGluAsn 129
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                                                                    75 LystysSerGinSerGluLysAspArgAla------
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NAME/KEY: misc_feature
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ROSENFELD, David
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                                                                                                                                                                                                                            1373 GGACCTGTGGCCGCTAGTGCTGGAGTCCATGCTGCACGCCAGGTGATGGATCAGAAGCT 1432
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                                  139 GCTGGGCCTCCTAGACTGTGTGACCTACTTCAGTGGCATCTCTGGCTCTACGTGGACAAT 1198
                                                                                1199 GGCCCACCTGTACGGGGACCCTGAGTGGTCGAGAGGGACCTGGAGGGACCTATCAGATA 1258
                                                                                                                                                                                                   145 sAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGlyIleArgGlnArgAs 165
                                                                                                                                                                                                                                                                                                   185 rProProCysProGluValGlnAlaLeuAsn-----ArgAsnLeu----- 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pThr---ThrLysSerArgLeuSerMetIleTyrPhe---GlyGlyProAlaLeuSerGl 284
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                                                                                                        rLeu------LeuLeuAsnThrAsnProAspVallleSerProLysSerLeuCysIl 125
                                                                                                                                                       125 ePheArgGluAsnProHisHisPheArgAlaValValGluAsnTyrIleThrAlaValLy 145
                                                                                                                                                                                                                                                    nThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPheArgLeuAsnHisTy 185
                                                                                                                                                                                                                                                                                                                                                 ------ValGlyPhe-----GlyGluHi 204
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            AlaGlyProPro-AspProPheGlyTyrGlySerLysArgIleGlyProAsn------
                                                          -------GlyAspValGlyTrp--------ValGluTy
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Sequence 34363, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICATY: WHI GENOMICS, INC.
APPLICATY: DeNISE, Sue K.
APPLICANT: KERR, Richard
                                                                                                                                                                                                                                                                             1433
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APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
TITLE OF INVENTION: COMPOSITION OF STEPHENCE: MAILLING-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR PILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 34363
LENGTH: 1535
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Mismatches:
Indels:
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|GCCAGGAGGCACGGGGTGGCGTGGCTGCAGGCTTCGGCGTTCAGTGATTG 9650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13294, Application US/10995561
Sublication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERENCE: CLOOUISS9
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER: OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13294
LENGTH: 15804
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Gly------ProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeu 294
                                                                                                                                                          652 GGAGGAGACGTCAGGCCGCAACTCTGCGTAAGGTTTTGCCCTGTAGCACCGTC---- 599
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Matches:
Conservative:
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OTHER INFORMATION: n = A,T,C or G,
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NAME/KEY: misc_feature
LOCATION: (1)...(15804)
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ORGANISM: Homo sapiens
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Best Local Similarity:
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US-10-995-561-13294/c
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